

```

1   CGGGCGCGGC GGC GGCGGCG GTGACAGCGG CGCCCGCGCC TCCCCGCGCG
51  TAGGTGTGCG GCGCGCTCCT GGCGAGGACG GAGCGAGCAG ATCTCGCGTG
101 CGCTCGCCGC CCGGCGCAGC CCAGCCCGGC CCCC GCCTGG CGCCCGGAGC
151 CGAGGTGTCT CCCGCGCCCG CGCCCGTGTC GCCGCGGTGC CCGCGAGCGG
201 GAGCCGGAGT CGCCGCGGCC CGAGCGCAGC CGAGCGCACG CCGAGCCCGT
251 CCGCCCGCGC CATGGCCACC ACGGTGACCT GCACCCGCTT CACCGACGAG
301 TACCAGCTCT ACGAGGATAT TGGCAAGGGG GCTTTCTCTG TGGTCCGACG
351 CTGTGTCAAG CTCTGCACCG GCCATGAGTA TGCAGCCAAG ATCATCAACA
401 CCAAGAAGCT GTCAGCCAGA GATCACCAGA AGCTGGAGAG AGAGGCTCGG
451 ATCTGCCGCC TTCTGAAGCA TTCCAACATC GTGCGTCTCC ACGACAGCAT
501 CTCCGAGGAG GGCTTCCACT ACCTGGTCTT CGATCTGGTC ACTGGTGGGG
551 AGCTCTTTGA AGACATTGTG GCGAGAGAGT ACTACAGCGA GGCTGATGCC
601 AGTCACTGTA TCCAGCAGAT CCTGGAGGCC GTTCTCCATT GTCACCAAAT
651 GGGGGTCGTC CACAGAGACC TCAAGCCGGA GAACCTGCTT CTGGCCAGCA
701 AGTGCAAAGG GGCTGCAGTG AAGCTGGCAG ACTTCGGCCT AGTATCGAG
751 GTGCAGGGGG ACCAGCAGGC ATGGTTTGGT TCGCTGGCA CACCAGGCTA
801 CCTGTCCCTT GAGGTCTTTC GCAAAGAGGC GTATGGCAAG CCTGTGGACA
851 TCTGGGTCATG TGGGGTGATC CTGTACATCC TGCTCGTGGG CTACCCACCC
901 TTCTGGGACG AGGACCAGCA CAAGCTGTAC CAGCAGATCA AGGCTGGTGC
951 CTATGACTTC CCGTCCCTTG AGTGGGACAC CGTCACTCCT GAAGCCAAAA
1001 ACCTCATCAA CCAGATGCTG ACCATCAACC CTGCCAAGCG CATCACAGCC
1051 CATGAGGCCC TGAAGCACCC GTGGGTCTGC CAACGCTCCA CGGTAGCATC
1101 CATGATGCAC AGACAGGAGA CTGTGGAGTG TCTGAAAAAG TTCAATGCCA
1151 GGAGAAAAGCT CAAGGGAGCC ATCCTCACCA CCATGCTGGC CACACGGAAT
1201 TTCTCAGTGG GCAGACAGAC CACCGCTCCG GCCACAATGT CCACCGCGGC
1251 CTCCGGCACC ACCATGGGGC TGGTGGAAAC AGCCAAGAGT TTAATCAACA
1301 AGAAAGCAGA TGGAGTCAAG CCCCAGACGA ATAGACCAA AAACAGTGCA
1351 GCCGCCACCA GCCCCAAAGG GACGCTTCCT CCTGCCGCCC TGGAGCCTCA
1401 AACCACCGTC ATCCATAACC CAGTGGACGG GATTAAGGAG TCTTCTGACA
1451 GTGCCAATAC CACCATAGAG GATGAAGACG CTAAGCCCG GAAGCAGGAG
1501 ATCATTAGA CCACGGAGCA GCTCATCGAG GCCGTCAACA ACGGTGACTT
1551 TGAGGCCTAC GCATTCTACT TCGAGAACCT GCTGGCCAAG AACAGCAAGC
1601 CGATCCACAC GACCATCCTG AACCACACG TGCACGTCAT TGAGAGGAT
1651 GCCGCCTGCA TCGCTTACAT CCGGCTCACG CAGTACATTG ACGGGCAGGG
1701 CCGGCCCCGC ACCAGCCAGT CTGAGGAGAC CCGCGTGTGG CACCGCCGCG
1751 ACGGCAAGTG GCAGAACGTG CACTTCCACT GCTCGGGCGC GCCTGTGGCC
1801 CCGCTGCAGT GAAGCCAAGG GAGGGGCACA GAATGGGGAA CAGGACACAG
1851 GATCCTAAAC TCCAAGGGGA CTGTCCACCG ATGAACACTC AGAGTGGACA
1901 CCATCTTCCG TCCACGCTGT GCCCAGGACA GCTGTCCCA TCCATGAACA
1951 CAGGGTAAAC ATCTGCCGGG CTCCGCACCA GTGGCTCCCT GGGCCATGGG
2001 ACAGCGGCAG GGCTCACCAC GGACAGCACG TGGCCCAGCA GCCGGCCACC
2051 CTGGCGTCCT GGGGCTCCTT CCCCTCCTCT CCCTCTCACC TTGTACCTC
2101 CACGGAGCTG CCTGTCTGGG ATAATTTGGG GATTTT TTTT TCTGGGGGAT
2151 AATTCTTTTG CATGACCCCT AAAGAGCAAG CCACACCGGT CTGCTAGCTA
2201 GGTGTCCGCG GTGTGGTG (SEQ ID NO:1)

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FEATURES:

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5'UTR:      1-261
Start Codon: 262
Stop Codon:  1810
3'UTR:      1813

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Homologous proteins:**Top 10 BLAST Hits**

			Score	E
CRA 18000005245285	/altid=gi 5326757 /def=gb AAD42035.1 AF07880...		1047	0.0
CRA 18000005199792	/altid=gi 10835006 /def=ref NP_001211.1 cal...		1044	0.0
CRA 18000004938668	/altid=gi 6671660 /def=ref NP_031621.1 calc...		1039	0.0
CRA 18000004937301	/altid=gi 11120682 /def=ref NP_068507.1 Ca+...		1038	0.0
CRA 18000005245287	/altid=gi 5326762 /def=gb AAD42037.1 AF08192...		1001	0.0
CRA 18000005171302	/altid=gi 3668373 /def=gb AAC79460.1 (AF085...		999	0.0
CRA 1000737074531	/altid=gi 6688228 /def=emb CAB65122.1 (AJ252...		986	0.0
CRA 18000005245288	/altid=gi 5326764 /def=gb AAD42038.1 AF08341...		986	0.0
CRA 18000004964693	/altid=gi 466360 /def=gb AAA81938.1 (U06636...		982	0.0
CRA 18000005199791	/altid=gi 4139268 /def=gb AAD03743.1 (AF112...		982	0.0

BLAST dbEST hits:

	Score	E
gi 12801212 /dataset=dbest /taxon=960...	1675	0.0
gi 12868201 /dataset=dbest /taxon=960...	1453	0.0
gi 2053138 /dataset=dbest /taxon=9606 ...	1247	0.0
gi 10213950 /dataset=dbest /taxon=96...	1243	0.0
gi 9324431 /dataset=dbest /taxon=960...	1233	0.0
gi 12921378 /dataset=dbest /taxon=960...	910	0.0

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

From BLAST dbEST hits:

gi|12801212 Fetal brain

gi|12868201 Fetal brain

gi|2053138 Testis

gi|10213950 Lung small cell carcinoma

gi|9324431 uterus endometrium adenocarcinoma cell libe

gi|12921378 Fetal brain

Tissue expression from PCR-based tissue screening panels:

hippocampus

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1 MATTVTCTRF TDEYQLYEDI GKGAFSVVRR CVKLCTGHEY AAKIINTKKL
51 SARDHQKLER EARICRLKH SNIVRLHDSI SEEGFHYLVF DLVTGGELFE
101 DIVAREYYSE ADASHCIQQI LEAVLHCHQM GVVHRDLKPE NLLLASKCKG
151 AAVKLADFGI AIEVQGDQQA WFGFAGTPGY LSPEVLRKEA YGKPVDIWAC
201 GVILYILLVG YPPFWDEDQH KLYQQIKAGA YDFPSPEWDT VTPEAKNLIN
251 QMLTINPAKR ITAHEALKHP WVCQRSTVAS MMHRQETVEC LKKFNARRKL
301 KGAILTTMLA TRNFSVGRQT TAPATMSTAA SGTTMGLVEQ AKSLNKKAD
351 GVKPQTNSTK NSAAATSPKG TLPPAALEPQ TTVIHNPVDG IKESSDSANT
401 TIEDEDAKAR KQEIIKTTEQ LIEAVNNGDF EAYAFYFENL LAKNSKPIHT
451 TILNPHVHVI GEDAACIAYI RLTOYIDGQG RPRTSQSEET RVWHRDQKW
501 QNVHFHCSGA PVAPLQ (SEQ ID NO:2)

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FEATURES:

Functional domains and key regions:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATION
N-glycosylation site

Number of matches: 3

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1 313-316 NFSV
2 357-360 NSTK
3 399-402 NTTI

```

[2] PDOC00004 PS00004 CAMP_PHOSPHO_SITE
cAMP- and cGMP-dependent protein kinase phosphorylation site

Number of matches: 2

```

1 48-51 KKLS
2 259-262 KRIT

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[3] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 4

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1 47-49 TKK
2 51-53 SAR
3 358-360 STK
4 367-369 SPK

```

[4] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 9

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1 36-39 TGHE
2 51-54 SARD
3 79-82 SISE
4 94-97 TGGE
5 109-112 SEAD
6 262-265 TAHE
7 400-403 TTIE
8 401-404 TIED
9 485-488 SQSE

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[5] PDOC00007 PS00007 TYR_PHOSPHO_SITE
Tyrosine kinase phosphorylation site

9-17 RFTDEYQLY

[6] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 3

1	302-307	GAILTT
2	332-337	GTTMGL
3	390-395	GIKESS

[7] PDOC00100 PS00107 PROTEIN_KINASE_ATP
Protein kinases ATP-binding region signature

20-43 IGKGAFSVVRRRCVKLCTGHEYAAK

[8] PDOC00100 PS00108 PROTEIN_KINASE_ST
Serine/Threonine protein kinases active-site signature

132-144 VVHRDLKPENLLL

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	195	215	1.665	Certain
2	319	339	1.301	Certain

BLAST Alignment to Top Hit:

>CRA|18000005245285 /altid=gi|5326757 /def=gb|AAD42035.1|AF078803_1
 (AF078803) calcium/calmodulin-dependent protein kinase II
 beta subunit; CAM2 [Homo sapiens] /org=Homo sapiens
 /taxon=9606 /dataset=nraa /length=542
 Length = 542

Score = 1047 bits (2678), Expect = 0.0
 Identities = 516/542 (95%), Positives = 516/542 (95%), Gaps = 26/542 (4%)
 Frame = +1

Query: 1 MATTVTCTRTFTDEYQLYEDIGKGAFSVVRRCKLCTGHEYAAKIINTKKLSARDHQKLER 180
 MATTVTCTRTFTDEYQLYEDIGKGAFSVVRRCKLCTGHEYAAKIINTKKLSARDHQKLER
 Sbjct: 1 MATTVTCTRTFTDEYQLYEDIGKGAFSVVRRCKLCTGHEYAAKIINTKKLSARDHQKLER 60

Query: 181 EARICRLKHSNIVRLHDSISEEGFHYLVFDLVTGGELFEDIVAREYYSEADASHCIQQI 360
 EARICRLKHSNIVRLHDSISEEGFHYLVFDLVTGGELFEDIVAREYYSEADASHCIQQI
 Sbjct: 61 EARICRLKHSNIVRLHDSISEEGFHYLVFDLVTGGELFEDIVAREYYSEADASHCIQQI 120

Query: 361 LEAVLHCHQMGGVVRDLKPENLLLASKCKGAAVKLADFLAIEVQGDQQAQWFGFAGTPGY 540
 LEAVLHCHQMGGVVRDLKPENLLLASKCKGAAVKLADFLAIEVQGDQQAQWFGFAGTPGY
 Sbjct: 121 LEAVLHCHQMGGVVRDLKPENLLLASKCKGAAVKLADFLAIEVQGDQQAQWFGFAGTPGY 180

Query: 541 LSPEVLRKEAYGKPVDIWACGVILYILLVGYPFWDQHKLYQQIKAGAYDFPSPWD 720
 LSPEVLRKEAYGKPVDIWACGVILYILLVGYPFWDQHKLYQQIKAGAYDFPSPWD
 Sbjct: 181 LSPEVLRKEAYGKPVDIWACGVILYILLVGYPFWDQHKLYQQIKAGAYDFPSPWD 240

Query: 721 VTPEAKNLINQMLTINPAKRITAHEALKHPWVCQRSTVASMMHRQETVECLKKFNARRKL 900
 VTPEAKNLINQMLTINPAKRITAHEALKHPWVCQRSTVASMMHRQETVECLKKFNARRKL
 Sbjct: 241 VTPEAKNLINQMLTINPAKRITAHEALKHPWVCQRSTVASMMHRQETVECLKKFNARRKL 300

Query: 901 KGAILTTMLATRNFSVGRQTTAPATMSTAASGTTMGLVEQAKSLNKKADGVKPQTNSTK 1080
 KGAILTTMLATRNFSVGRQTTAPATMSTAASGTTMGLVEQAKSLNKKADGVKPQTNSTK
 Sbjct: 301 KGAILTTMLATRNFSVGRQTTAPATMSTAASGTTMGLVEQAKSLNKKADGVKPQTNSTK 360

Query: 1081 NSAAATSPKGTLPAALEPQTTVIHNPVDGIKESSDSANTTIEDEDAKARKQEIIKTTEQ 1260
 NSAAATSPKGTLPAALEPQTTVIHNPVDGIKESSDSANTTIEDEDAKARKQEIIKTTEQ
 Sbjct: 361 NSAAATSPKGTLPAALEPQTTVIHNPVDGIKESSDSANTTIEDEDAKARKQEIIKTTEQ 420

Query: 1261 LIEAVNNGDFEAYA-----FYFENLLAKNSKPIHTTILN 1362
 LIEAVNNGDFEAYA FYFENLLAKNSKPIHTTILN
 Sbjct: 421 LIEAVNNGDFEAYAKICDPGLTSFEPEALGNLVEGMDFHRFYFENLLAKNSKPIHTTILN 480

Query: 1363 PHVHVIGEDAACIAYIRLTQYIDGQGRPRTSQSEETRVWHRRDGKWQNVHFHCSGAPVAP 1542
 PHVHVIGEDAACIAYIRLTQYIDGQGRPRTSQSEETRVWHRRDGKWQNVHFHCSGAPVAP
 Sbjct: 481 PHVHVIGEDAACIAYIRLTQYIDGQGRPRTSQSEETRVWHRRDGKWQNVHFHCSGAPVAP 540

Query: 1543 LQ 1548
 LQ
 Sbjct: 541 LQ 542 (SEQ ID NO:4)

FIGURE 2, page 3 of 4

Hammer search results (Pfam):

Model	Description	Score	E-value	N
PF00069	Eukaryotic protein kinase domain	306.2	3.9e-88	1
CE00022	CE00022 MAGUK_subfamily_d	293.8	1.3e-86	1
CE00359	E00359 bone_morphogenetic_protein_receptor	15.0	0.0015	1
CE00031	CE00031 VEGFR	0.9	2.1	1
CE00287	CE00287 PTK_Eph_orphan_receptor	-65.4	0.00046	1
CE00292	CE00292 PTK_membrane_span	-77.0	0.00018	1
CE00291	CE00291 PTK_fgf_receptor	-93.1	0.0021	1
CE00286	E00286 PTK_EGF_receptor	-132.2	0.0059	1
CE00290	CE00290 PTK_Trk_family	-161.3	0.00033	1
CE00016	CE00016 GSK_glycogen_synthase_kinase	-196.7	9.2e-06	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
CE00359	1/1	132	186 ..	272	327 ..	15.0	0.0015
CE00031	1/1	133	205 ..	1068	1139 ..	0.9	2.1
CE00286	1/1	14	252 ..	1	263 []	-132.2	0.0059
CE00290	1/1	15	253 ..	1	282 []	-161.3	0.00033
CE00291	1/1	14	267 ..	1	285 []	-93.1	0.0021
CE00292	1/1	14	267 ..	1	288 []	-77.0	0.00018
CE00287	1/1	14	270 ..	1	260 []	-65.4	0.00046
PF00069	1/1	14	272 ..	1	278 []	306.2	3.9e-88
CE00022	1/1	10	305 ..	13	316 ..	293.8	1.3e-86
CE00016	1/1	1	343 [.	1	433 []	-196.7	9.2e-06

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1 GAGCTGCTGT GTCTCTGTCC CCAGGGGCGAG AGGGGCTGTG GGGTTGCAGG
51 CTAGCGTCT GGGACTCTGG GGTGAAGGCT CAGCCATGCC CTGCAGACAC
101 CATGGGGCAG GGCTCAGACC TGTGCACCTG TCTCTTGCAA ACCACTGTTT
151 TCTCTGTTTT GTAACCCCC ACCCAACCCC ACATAACACC TCTGGGTTTA
201 AACACATGC ACCCTTGTGC CGGTACCTC CCTGCAGCCG GAGAACCTGC
251 TTCTGGCCAG CAAGTGCAAA GGGGCTGCAG TGAAGCTGGC AGACTTCGGC
301 CTAGCTATCG AGGTGCAGGG GGACCAGCAG GCATGGTTTG GTGAGTGCCA
351 GGGGCAGGGT GTGTTGGCTG GCAGTTGGCA GGGCAGGAGG TGATGCTGAC
401 AGCCCTTGT GGCCTCTTCC CCTCTCTCTA GGTTTCGCTG GCACACCAGG
451 CTACCTGTCC CCTGAGGTCC TTCGCAAAGA GCGTATGGC AAGCCTGTGG
501 ACATCTGGGC ATGTGGTGAG GCCTGGCCTG AGTTGGTGCG GGGCAGGGCC
551 TCGGGTGTTT CAGGACTTCC CACCTACATC CTGGAGTGTG CAGTGGCCAG
601 CACGTCTTGC TCTCATCTGG GTTTATCTGT GTCAGACCTG CCCTTGAGCT
651 GCCCTGGCAG GGGTCTGCCC ACACAGCCAA GAGCCCCCTT TCCACCCAGA
701 TTAGAATTGC TCACATGAAC CTGGCGCACC CCAGTGCTCG CCTGCGCTCA
751 GCAGAGGTCT GGTCCAGAAG TGTGGTGGGT GGATGGGAGT GGAGAAGAGA
801 GGTCAGGGGC TGTGGGGCCA TGGGCAGGGC CACCTCCTTG GGTAGGGGTC
851 TCCTCCCA CAAGGTGGGA GCAGCAGAGG GGCTTGACAT CACCCTCATC
901 CCTGTGATAG TGTGGGTGTG GGCAGAGGT CAGGGGGCCG GCTGTGCCCT
951 TCTACCCAG TGTCTGTGC ACAGGTGGGG GCAAAGGAAT GCTGAGGACC
1001 CCAATGCCCT CCCAGGGCCA CAGGAGCTAG GCAGTGAGGG TGCAGGGCAT
1051 GGGCTTCATG GACGGTGGCA CCCTGCAAGT GGCTGCGGTG CTCACAGGCC
1101 CCATCCGCGAG GGGTGATCCT GTACATCCTG CTCGTGGGCT ACCCACCCTT
1151 CTGGGACGAG GACCAGCACA AGCTGTACCA GCAGATCAAG GCTGGTGCCT
1201 ATGACGTGAG TGCACCAGCC CCTCTCTGAT GAGCTCCCTT CCTCCAGGTG
1251 TGGCCGGGTG AGGGCAGCGT GGGAGAGGC TAGGAGTGGG GTGAAGCCAC
1301 CTGTGGCCAG GTCCTGGGTC CTGCTCTCCC AGATTCTGTG CTGGAGATGA
1351 AGCCCTTGG AGAATTCTTG CCCCTGCCTG AGAGGGAGCT TCAGGCCCGG
1401 CCGGGCGCTG GTTCTCTTCT GCAGTTCCCG TCCCTGAGT GGGACACCGT
1451 CACTCCTGAA GCCAAAACC TCATCAACCA GATGCTGACC ATCAACCCTG
1501 CCAAGCGCAT CACAGCCCAT GAGGCCCTGA AGCACCCTG GGTCTGCGTG
1551 AGTCGCCCTT GGTGCCCATG GTGGGGAGGG GGCTCCTGGT GGAGATGGCC
1601 TCAGACCACT CCCCTGGCAA GGACCCAAAG AGGGTCTGT TCCTGACATC
1651 CAAGAGCTCC CTTGGGTCCC CTGGGTGCTC CTTGTGGCCT CTGGCTTGGG
1701 ACATACCAGC ACGTTTGTGA GGCCTGGGGC TTGGAAGGCA TTAGAGGGTA
1751 GAGGTGATCC CTTCCCTCCA ACTGCAGTCC TGTCTGTGAG GGCAGAGTG
1801 GACGAGGCAA GGGAGAGACG AGTCTTGAAG TCCCAGGCGG GTGGGGACAG
1851 ACAACCCTTG CCGCAATGGT GGCCGGTGGC TCTTGCCAAG TGGGGACCCC
1901 AGGGTGCCAC AAGCCTTGCC ACCCTGGCCT CTCCTCTGTG CCTCGGGCTC
1951 GGCTGCCATA TGACCACCCA TTTCCCCACA GCAACGCTCC ACGGTAGCAT
2001 CCATGATGCA CAGACAGGAG ACTGTGAGT GTCTGAAAAA GTTCAATGCC
2051 AGGAGAAAGC TCAAGGTGAG GCCCTGGCCC CTAGTCCCAG GCACGGCCAT
2101 GCTTCTCTGT GTCCCCTTGG GCTGGAGCAG GGGGGCCTTG GGGGGTCTGG
2151 GCAGACCTAG GGGTTACTGC TGCCCCAAG ACTGACTGTT AGCAAGTCCC
2201 AGACTGGATG CATCAGGTGA ACTCAGGCCA GCTTGGGAAT GAGTCCAGAG
2251 GGGCCCTGGG CCAGGTGTGG CTCCTCCTAG TTGTCTGTGC CACCTCCTAG
2301 CAGCCCTTGG AGGAGCTGTC CTGAAGCGCT CGCTGTGGGC TCCTACCCG
2351 GGCTCTGCAG GCAGCACTCA CCTCTGGCA GTCACACTGT TTAGTACAAG
2401 CAAGTCCGAA GCTTCCGGCT CAGACAGGTT TGGTAAGGAG AGCAGAGCCA
2451 CACACACTGG TCTTGGGTGG GCTGGGGGAG TTCTGGGAGG GAGGTGGGTC
2501 CCAGTAGGGT ATCCAACCTG CCTGCTTTGG TCAGGGCTGG CTCCGGTGAC
2551 CGCACACTGG CAGTCCCTCT ACTTGTGGGT TCCGGGATGG GGACTTGTG
2601 CCTGACTGCC CTCTGCTGGT CTCTGAGCAG TTCTCCCCGG AAGCCCCAGG
2651 ACTGTTGCCC TGTCTGAGCC TGTGAGGAAA AGAAGGGGCT GTCAGGGAGC
2701 TGGACCCAG AGGAGCTGCC GTGGTGACCA GCTGTTCTGG TGACCCCTGA
2751 GGCTTGAGGG GTCTTGAAGC AGCTAGAAGC TGTAAGTGGT CAACAGGTTT
2801 AGGCCCAGGG TGTGTGTAGT TCTGGAAATA GGTGATCTGT CTCAGTCCGG
2851 CTGCTGGCTT CCTGGAGCTC TTGCCTCTCT GGAAGGCTGA GGTATGTCA
2901 GCCTCATGAC AATGAGGCTG AGCATCTGGG CAGGAGGACA GGGGTCTTAT
2951 CCTGCCCAGA AGCCAGCAGG GAACACTGAT GGGATAGCCC CGGTTTTATC
3001 TGTGTCTCT CCCAGGGAGC CATCCTCACC ACCATGCTGG CCACACGGAA
3051 TTTCTCAGGT GAGCCTTTCT TCTCCAGGGA GACAGGCGCT GCCCCCTCCC
3101 TGCTGGCCCA CGCAGGAGAG CGCCTCCTTC CTCACCAGCC TCTCCACTCC

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FIGURE 3, page 1 of 16

3151 TCCTCTGCGG CAGGCCTGCC CTCGGCGTCT GCCCTCAGCT CTGAGACCCA
 3201 CTGCCCCACCT GGCCCCGCTG GGCTCCCACC TTGGGTGATA CCACAGGGTC
 3251 CAGCCCCCCC AGGCCATCAC CTTCTGTCTG GGTCTGTGTC CCTCCACCCC
 3301 CTGAACACGA GCGTCTGTGC TGCCCCACTG GGGCTCACAG CATCGTGTGT
 3351 GTCTGTCCAG GCGTTTGTGC GGCATCTATG TGGCTCCTT GTCATTTTGA
 3401 GTGCTCTGAA CATTGTGTTT TGTGCGGGAG GTGGGCAGAA GGGATGCGGG
 3451 GTGATGCGGG AGGCTCGGGG GCCTCCTTCC AAGTTCTGGA TGAGCTGCAG
 3501 CCTCCTGTCC CGGCTGCTCA GGGTGGGTGG TTGGGAAGCA AGTTCTCTTG
 3551 GCAGGGGGGT GGGGTCTGTT ATAGACCCTT GAGGCCAGG GCGCTGGCAG
 3601 ACCCATCGGG GCATGATGTT AGCCCCGAG TGGAGCCGGC AGCCAGGGTC
 3651 TGGACAAGCT GTACCTGTGG CTTCTCCGTC GTCCGACACT CCGTGTGCGA
 3701 GCGTCTGTGA TCCGTCTCTC TCGTTGTCCG TTTGCATCTG GTGCCCCCA
 3751 CCCGCCATCC TGTTACTTTT GCTGTGATGC TGTAATGCCG GGAACGCGTG
 3801 CACACGGTCA CACCAACACT AATAGGACTG TCCTGTCTGC TGTGTGCTCA
 3851 CCACACCCTT TGGGCAAGAG AAGCCCCAC TGGGGTTTTC TAAGGAGAAA
 3901 GGAGGCAAAAT GCTTTTCCGT GTCAATCAGT CCAATCTTGT TTTCACTCTC
 3951 TTGAGCAAAG GATTCTGGAA CCATCTGTCA CCTAAACTTT AACTCTAATC
 4001 TTCTTCTGCT TCCTTTGTCT CTTTCTTCC CTTACCTCGC CCACCCCTCG
 4051 TCTGTGTCCG CCCACCCCTC CCTTCCCCTC GTCTCTAACC CCGTGTAAAC
 4101 AGTGGGCAGA CAGACCACCG CTCGGCCAC AATGTCCACC GCGGCTCCG
 4151 GCACCACCAT GGGGCTGGTG GAACAAGGTA GATGTGTCTC GACCAGCGTC
 4201 CCGCCCGCTC CCGCCCGTCC CTCCTGCCAG CATGCAGCCC CCGTGTGCAC
 4251 GCAGCGGCTG GCGGGGCTCC AGAGCCGCCC CAGAGGCCGC CAGGCCCCCG
 4301 GGAGCCCCTG CTCCCGTGTG GTCACATCCC AGCAGAGCCC ACCACAAGGG
 4351 CAGGGAGGCA GCCCCAAGG CTCCTCGCCT GTAAGAGGAG GGGCTGGGCT
 4401 AGGTGCCCCC TGGGCTACAC CAAGCCCTTC TGGTCTGTGC CCCCAGAGTC
 4451 TGGGGTCCG GAGACCCCA TTAAGAATGG CCTGGGCCCC ACAGGGAGCC
 4501 ACTGGGCTG CTGCTGGGGG GTCTGAATCC TGAAAGGAGA GCCTTGAGGA
 4551 GCAGAGCCAG AGAGGCAGAG GCCCTTGGGG CAGACACACA CCCTGCCCTT
 4601 CTGGGGCCGC ATGGAGACGG TGGTCTGTGC TGCTGAGTCC TACACATGCA
 4651 TGTCTGCCCT GAGCATCCCC CCAGGACAAG CCGCTCTGGA GTGGGTGAGG
 4701 GTTTTATGCA CCCTGAGGAG ACTTTCAGG CTTCCTCTTG GGTGTGTTCT
 4751 GCAAAGTCTT CCTCCCTGG CCTCAAACCC TGTGAGGGAA AAGGCCGGCA
 4801 CTGGCCACCT GCTCCTCTGG GCTGTGCGGG GCCAGAGCCC AGAGGCCCAA
 4851 GTTGGCTTCT GCCCACCTGC TGGCTTGTGA CCATGGGCAG ACCCATGAG
 4901 GGCTAGGCGA CCCCAGACC TCCTTGACG TCCAGCCTGA GCTGAAGGCT
 4951 GGTGAGAGCT TAGGGCAGGC CAAGCTGACA ACGCCTGGCC ACAGAACACA
 5001 GAGGGCTACA GGGGTGACCC CAGATCCTCC CTGGGCTGAG CTGCTGAGTT
 5051 CCCTGTGCGT GCCTCCAACG TGGGCTGGGG ACCCGGCAGA GGTTCCAGGG
 5101 TGCTGGAGAC TGCCTTCCCC AGGCCTCCTC ATGACCCACA GGGTGAGCAG
 5151 CCTGGCCTTC CCAGCCAGAG AACCTCCTT CTGGGGAGGC CCAGGGCGTC
 5201 CTCGGGGAGG GCAGTCTATT CTCTCCCAT GAGCCAGTG GACGTGTCTA
 5251 GCAGGCAGCA CCCCAGGAGA GCCCTCCAC GTCTTCTCCA TTTGACAGGC
 5301 CTTTCCAGAG CGCAGGCGGG AGGGGGCTGT GATTAGAAAA GAGTGAGGCT
 5351 AGTGGCTTCT GGGGAGGCAC TGCTGCCCAG GGGACAGTGC TGAGAGACAG
 5401 CTGCCTCTAC GCTGCCCTGT GCCCGGGGCT CCCGCTGCAA TGCCCGCCTG
 5451 TCTGCAAGTG AACGTGGGGC GACGGTGCAT GAGGCCCTGC ATGTGTGGCT
 5501 CCACCTTGGG CGCCGAGAGC AGCTCTGTCC TGGAGGGTGG TCAGTGCATG
 5551 TGGACAGAGC CCAGCATGGC TGTCTTGGGT GACCAGCTAA GGGGACAAGG
 5601 CAGAGGCAGG GCTGAGAGGA CCACCCATCC TGCTAGGTCA GCCCAGCTCA
 5651 GCCATATCAC ACGGCAGTGA GCATGGAGCT CAGTTCTCTG CCAATGGCAG
 5701 CTGAGTCTAG TACCATCCAG TCAGAGTCTG GTACCAGCCC ATGTGGCATA
 5751 GCCCCCTCGG CCCGAGAGA GACCCGCTT GTCGAGTGTG CTTCAAGTTG
 5801 GCCTCTGTGG TCTCTCCTGC ATTGATCAGG TGTAAGGGCA TAGGAGACCC
 5851 AGTGTCCGGC CAGCTGCAGG GTGGCAGCAG TTGCCCGGC CTGGAGACCC
 5901 GGGAAATGGG AGTGCCTTCC CAGGATGGAG GGCAGAGGGT CTCTCCTTGT
 5951 CCCACAGAGG CCTGCAGAAC CCCCACCCA GGTGTCTGAG ATGCCTGTGA
 6001 CTGCTCCGCC TACCCTGGGC TCCTGCGGCA CCTAACGCAT GCTTTGAACT
 6051 TGAGACACAG AAAGGAAGTT CCCGTGCCCT TGAATGCTAG TGTAGATGGG
 6101 CATCGACAGG ACTCTGGCCA CCGTGAATCT GGAGTTAGTC CCAGGCAGAG
 6151 ATGTGAAATG AGCAGCCCCC CAAAAATGG TTGGCCGGGA GCCATGCACT
 6201 CAGGAGGGCC GGGCCCATGC ACCCCACACT GCGCCCAAGG CGTGACAAAG
 6251 CGATTGTTTT AAAAGCGGGT TCACAAGGAA GGATGTTTGG GAACTGACTG

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6301 AGACAACAGG GACGTCTGCT GCAGGGCTTC CCAGAGCTCT GATGGCAGCG
6351 TCGGCCTGAG TCCCTTCGAG AGGGCTGGTT TGTACGTGGC ATTTGCTGCC
6401 CACTGGACTG TGAACCTCTG TCTTTTATT TCCACTGCT GCTGTGGTAC
6451 ATCTCCAGTA GCATAGTTTG GAAATGCAGG TTTTGATAGA CTCAAGGATC
6501 TAAATAGAAC CCTCTTAGTA CCAAGGACTG TCCGGGGTCT CTGCCAGCCC
6551 CGCCGATGGG CCTAAGTGTG GTGCCTCCTT TCCTGTGAGA ATCTTCTGAG
6601 GACATGCCCC GGGAAAGAGC TCAGTTCTGC TGCTGCCTAG GGTGCCATGC
6651 TGGCCCCGGT TCCAATGCAG AGCCTAGCTG GAAGTACCGC TGGGTTGGCG
6701 GAGGTACGT GCCTGACTGT CCCCTCGGG GTGGGGTGGA ACTAGCCTTC
6751 TGAAACCGCC TGCTTCAGTT GGCCACAGCT TTTTGAAATG TGTGTTTCTG
6801 GAAGGGACTG GGTCCCTTCC TTGCCTGTTT AGCTCCCCAC GACAAATGTC
6851 CTCAAGGCGA GGCTGGATGC TTCTTCCTC AGGCTCCTAG GAGGAGCCCG
6901 TCCCCAGCT GTGTGCGGCA GCTGCTCACC AGCAAGGACA GGATCCCTCA
6951 GCTGCAGCCT CAGGCTGGCT GGCCTGGGC GGGTGTCTTCT GGGATGAGTT
7001 GTGTGTACTG GAGATGGGAG GGGAGCTGAG AGGGTGGGAT GCACAGACAG
7051 GAGAGGGGAC TGTGGGGTCT CTGGAACCTT GAGTTCCAAG TCTTCAGGAC
7101 TCCTCCCTCA TAGCAAGTTA CAGGGAAGCA GATTTGAGCC ACAGGGAAGC
7151 AGATTTGAGC TGCAGCGAGG GGGAGGGTTT TCAGTCTGTG CTATAGGGAA
7201 GTGGGCAGTC GGCATTTCTG GTCCTGGGAA CTCCTGGGC AGGGCTGCCT
7251 TGGGACATCA GGGAGGTGGC GCTGTGCTCA GCTTCACCAG GAGGGGCCTT
7301 AGGCCTGGGG ACGGAGAGTG ATGCCTGAGG CCCCTCTACT TCTCCATGGA
7351 TCTGGGAGG GACTCCTGGG CTGGATACAA AATTGTTGAG AGTTAAGAGA
7401 TCTGTGAGGA GAGGGCAGCT GGGGAATAGAA AGTGTGTGCC CACTGCACAT
7451 GGGGTCCGCA GGGCCACGTG CAGCCACTGC GCAGGCACAA CCCCAGTCCC
7501 CACAGAGCCC AGGAGGGGCC AGAGCCATGG AGGAGGCAGC ACTGGGCATT
7551 TGACAGGGA GGGGGTGGTC AGCAGGCAGC AGGCCAGGC CTGTCTATGC
7601 CTGCGGGGT GCAGCCTCCT GATCTCCACG GCAACCTGGA GCACCCAGCG
7651 TCAGAACCAC CGGGAGGGCT TATGGAACAG ATGTCCAGCC CTGCAGAAGT
7701 TCTGGCTCAG GAGGGCAGGG TGGCCTGGG AATTGTCATT TCTGACTGTA
7751 CAGGGCGATT CTGCTGCTGC TGCTGCTGCT GGGGTGGGG GAGGATCCCA
7801 TTTGAGAAGC GCTGCAGTCC TAGGTTGAAA CGTGCCTGTC TGTCCCCACC
7851 CAGGCTGCA TGGGCAGCAC GGGATCCCCA GGCAGGAGGA CCCAATTCA
7901 TGGCCTGGCC AGCCAGGGTC CTGGAGCCAG GCGGTGGGG AGGGATGGGG
7951 GATTGCTGTA CCACCTTCC TCCCGGCTTG GCCCGGGGC AAGCATCCTC
8001 ACACCTTCCA TGTCGTATC CCCTTGGCTC CAGCCTGGCT GCCTCTCTAA
8051 CCCTGCTGTA CCGGCTGGCC GCATGGCCCT GGCTCTTTT GGTGAGCGTG
8101 GTCCAGGACT GGTGACCTGT GAGTCTGGG CCCGCAGTCT TGCGCCCCCTG
8151 CCCGAACCAA CACAAATCTT GTTTTCTCTC TCTCTCTCC TCCCTCACTC
8201 CCTCCCCTTC TCACCTTCTC TTTTCTGTAA GGTAAAGCTGA CTTCCTCTTT
8251 TGGTTTTTTA TTTATTTTTA TTTTTTAGTT CTGTAATTAA AATCCTAACA
8301 GCCATGGAGG GTGTGGGCAC CGGGGGCTGG GGCCAGGCC CTCTGACCTC
8351 TGAGGGGGAA TGCTGGGTGA GGCAGGGGCC CCGCTGCTGG GACCAAGTAT
8401 CCTCAGGGGC TTGTGGGCAG AAAGGCCTGT GCTGGCCCCA GTCAGTGCAC
8451 AGAAGCGGCC CCAAGGCCAG GGCTGCTGGG CAGCTCGGAA TGAGGGCGAG
8501 CAGGGCTGCC CTTGGTGCCT GAGCCAAGGA GCCAATGGGA CAGACCTCTG
8551 AGCCTGGGTG CCAAGTATGA GGTCTGAGAC AGGGTGAGCG CCTGGGCTGG
8601 GACAAGGCC TCTGAGTGGG CGGCCAGCTG CAGCCCACC ACCCTACCC
8651 CAGGAAGGCA GGGCCCGGGA GGGCATGACC TCTGGGGTGC TGGCTCAGCT
8701 GCCCCACCC CAACCTGACA CCGCTAGTCC TGAGTTCCCA TCAGGGAGGA
8751 AGCAGCATCC TGCTTCTCTC TAGGAAGAGC TTGCATGTGG CCCAGAAGCC
8801 AAGGGGGCTC CCCAGCACCC ACGGGCATCT CTGGGTCTGG TCAGAGGAGA
8851 AATCTGGATG CTTGCAGGAG CCCAGGGTC ATGGAGGAGG CTGGAGACAG
8901 GGCTGTCTTG GGTGATGGG ATGGCCCCC CACCTGCTCA GAGCCAGCCT
8951 GGGTCTGGGA ACCACCTTG CCTCAGGACC CTGGGCTTGC TCCTGGGGAA
9001 AGAGTGGGGT CAGGCAAAGG GGTGGGGTTG CGCTGCAGCG AGACCCAGGC
9051 CCATCACTCA CCATACCTTC TTCCTCCCCA TGCAGCAGCC AAGAGTTTAC
9101 TCAACAAGAA AGCAGATGGA GTCAAGGTGA GGCTCCAGCC GGGCCCTGTG
9151 GTGCCGGGGA GCCCAGAGCC TGCAGCTTCA CCCCCACGCC CTGGGGCTCC
9201 TGCTCTGGAG TCCCCCTCCC CCCATGCCCT GAGAGACACG GGACAGGGAA
9251 TGGCGAGTGA GGGGCTTCTC CCACCTAAGA GTTCTCTTTC CCTCTCTCA
9301 CAGCCCCAGA CGAATAGCAC CAAAAACAGT GCAGCCGCCA CCAGCCCCAA
9351 AGGGACGCTT CCTCCTGCCG CCCTGGTACT GAGCTCCTCA AATTCTGCCT
9401 CTCAGCCCCC CTACGCCCC TGGCTGTGTG ATTGCGGCTG GTCAGAGGGG

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9451 GCCGGGTGAA GGTGGGTCT GGGCCGCCT GGCTGTCTG ACAGCACTCG
9501 CATGGGCCCC GGGGCTCATC CCTCACCAGT GGTGAAGTGG AGAGAAGAGG
9551 CCACTGTTGT GGGGGGCTCC AATTCAGACA GGTTTAGGAC TGCTCTGGGG
9601 AGCCCCCTGGC TGAGACCCAC AGATGTTGGG GTGCAGGGGA GAGGCCCAGC
9651 CTCCCACCCA TGTGTACTTG TGGATGTCTC TCCAGGAGTG TTCAGGAAGT
9701 CAGTGAGGCA GAAGATACCC TCTCCCCACC AGGACCCAC CCTCAGCTCC
9751 TCCACCATCC TCAACAGGCC GACCCACAGA CCACTCCGAA GGTCTGGCTT
9801 GGTGGGGCTG GGCAGGATC TGCAGGGGA ACAGCCATA GTGGCACATT
9851 CCACGGCCCA TGGGGAGACG GGGCCACGGT GGTGCAGTAG AGAGGTGTCT
9901 AAGCCAGTGG CAGCCAAGGG GAGGGCTTGC CGTCACCTCT GTGTTCCCTC
9951 AGTGCTGCTC TGTGGCTGCC TGAGAGGCAG GGCTTAGGGG CTCCCTGCCG
10001 GGGAGGGGAG GGGTCCCCAC CATGCTCCGC TCCAACGCG CCCCTCAGTG
10051 CCCCTTGCCC TGGGGGCTCC TACAGGTGAA CCCTATAGCA GTACTCCCAA
10101 GGATGTAAAG TTGTGGCTGG TGGGTGCCGG CCTTCCTGCT GGGGCGCTGT
10151 GCTGTGTCCC CTCAGCTGTC CTAAGAGCTT TGGGGCTTGC TGGCCCGTAG
10201 GTCCCCATAT TTGCTGGAAG CAGGCTTGGT GTCCCCTGAG AACCCAGGC
10251 CAGGCTTCGG GAGCCAGCCC CAGACCGCCC ACGGGAATAC TGGGTTTGCC
10301 AAATGGCCAC CTTGAGACCC AGGAGAGGAG AGCGGTCTCT GGAGGGGCGA
10351 GCTGCTCAGA GCAGCCAGGC CGTGGCTGGA GGGTGGCCTG GTGCAGCCTA
10401 CCTAGGGCCT TCCAGTGGCC AGGGCAGCCC ACGTGCCAGC CTCACAGCCA
10451 GCCCCATCTC GGACCCTGTC CATCCCATGT GCCACCGCCA CCCCATGAC
10501 ATCTTCAAAC CTGTGCCCCC CACCACGCTG GGGCACAGGT TCAGGCAGTA
10551 AAGGGTAGGG AGAACCCCTC AAGACCGAGC CTGGCTTCTC TGGCTCCAC
10601 ACACATTGTG CAGCTTGTCT GGGCCCCACA CGGTCCATCT CCCACCCTGG
10651 ACAGCAGCAC CTCGCGCAGC CTGGACAGAG CTCCTGTCCA TTCCATCCCT
10701 GCCGGCTGAC CCAGGCTCCT CCCCCAGCTG CTCCACGCGC CCTCCATCCC
10751 TGTCGCCAC TCTGCTCTGC ACTTCTTTCT CGCAGGCTCT GGCCACCCAC
10801 ACCTCCTCTG TCTCCCTGTT CCCCTCCTGG TGGTCTCCGC TTCCTCCTCT
10851 TCTCACTTTC CCTCTCTTTC CTTCCTCTGT GTCTTCCTTC TTCTGTAGGA
10901 GCCTCAAACC ACCGTCATCC ATAACCCAGT GGACGGGATT AAGGTACTGC
10951 CCCACTTTCC TCCTCCCGCT TTCCCCAGGC AGGAGGCTCC AGGCCAGGAG
11001 AGAGGTCTGG GGCAGCATTT GTGCCAGAGT GGAGGGCAGA TGTCCCATGG
11051 CCCTGCGCGC CCCTCCCCGC AGTACGGTAG GGCCCCAGTC CGTCTTCGTG
11101 GGCAACAACA GGACAGACTG GCTCAGGCCC CAGGCGCGCC CCTGGAGGTG
11151 CTTGGCACAG TTGCGCCCGG TCCCCATGTG GCCGACACTC TCAGACCAGG
11201 GCTCTGCGTG TCCCACCTAC GGCAGGCAGT AGGGCTTCTC GAGGTCTGGA
11251 GCAGGGCCTG CATCTCAGGA GCTGCATCCT TGGCCCTCCT GGCTGTCTCT
11301 CACCCACCT CCCTCAGTG GCCCCAGTG CTTCCTGCTG AGCAGACCCT
11351 CCCTCCTCTG CTCCCCTCTC TGCTCTGGCC ATCAGCTCCC ATCACATTGG
11401 CATCATCACT CTGGGGCCAG GGAAGGGGCT GGCTCTCTGG GGTGGTGGGA
11451 GGGATGGGGC CAGCAGCCAA GCCATTTCCA GGACTTCCAA AACAGCGCCA
11501 CTACACCCA CACGGCCCTC CAGCCAGCT CCCACCTAGG CCTGGGCTCC
11551 TTACAGAGCC CCCAGAGTGC CTCTGTGGGG ACCCCCCACT TCCTTCTGGC
11601 CAGTGCCACC ACCCAGCCCA TCATCAGAAG ACATCTTTCT CCATGGCAGG
11651 GACCAGGGGG TCCAAGGGGC ACCCATGGTG CTAGGCACCA GGGCCTGGGC
11701 ATTCTTCCCA TCTGGCAGCT GGGGATGGGT GCCCTGGGA CCCGTGTGTG
11751 TCTGGGGTGG GTCATGCTCT CTGCAGGACT CCTAAACAAC CTTCTGGGCT
11801 GTGGTGAAC CTGAGCCTGC ACCTAAAAGA CCTGTAGTTC TGGTCTAGGG
11851 CCTCCAAGCA GTGTCCAGGC AGTGTCCAGA CCAGGGGGCG GTCCCCCAGG
11901 GACCTTGTA GATGTTTCCT CTGAGGAGCA GAGCAGGCCT CCTGGGGACC
11951 TGGGGGATGG TCTTTTGAAG GGCAGCAGCC CTGGAGCAGG GTGGGAGAGT
12001 CTGGGGCCAC CTCTGCCCTC TAAGGCCACC TGAGAGGTGA GGCCGGGGCC
12051 TGA CTGGACG TCCAGTCCCA GAGGGGCGAG TGCCCTGAGG GAATGTGGGC
12101 GACAGGAATG CTCTGCCTGG GGCCAGGCCA AGGTTCTCTG AGCCCTGTGC
12151 GGATCTGCAG AGCTCCTGGG AACGCCTCAC CCTGTATTTT GGATGACACC
12201 GGCTGCTGCT TCATTGGAAC CAGCCAGTCC CATTTGTGTT TACGTCTTGG
12251 AATTTCAAAA AGCCCATTTT CCTCTCTTGT TAAAGAGTCA GCTGAGCATA
12301 CCAGTCTCTC TGCCAGGCTC ATCTTGCTGG GAGAAGTGGA GCCCTCATGT
12351 GTTGGGGATG CAGGGTGGCC ACAGCACTAG GGTGGCAGGG CCGGCCTCGG
12401 ACTCCGTGCC AGCCTGTGCT GGCTGCCGTG AGAATGCACC CTGGTGAGGG
12451 GCGCCCTCCC AGGGACCAGC ACAGAAGTGG GTGTCTTCTC CGGTCACTGC
12501 CGCATGAGGT CCACAGAGCT GGGGCCCTGC AGCCGCCAGA GGGCATGTCC
12551 CCTGAGCCCC TGGCCTTTAA GCCCCGTGGA AGCAGCCGAG GCAGAGATCA

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12601 GCTTCAGAGC CTGGGCTGGT CCTGACACAG GCCCAGCCCT GTCCACCTGC
12651 CCTCAGCCAC GTCCCACCTA TCCTTGGCCG CATCCTGACC CGCTGCCTCC
12701 CGTGTTCCT CAGGAGTCTT CTGACAGTGC CAATACCACC ATAGAGGATG
12751 AAGACGCTAA AGGTACCTGC ACTTGAGTCC TTGCCCCCCC AGCGGCCTTG
12801 GCATTGCTGG GTTGCTCTTT GAGGTGGGTG GGAATTGGGC AGGGTCAACT
12851 CTCTGCGAC GCCTAGTTTA TGCATGTGTT GAGGGGCTCA GGGACCCTGT
12901 AGCTGTAATC CTGCTCCAAG CCTGGGTGTC AGGCCTGCCC AGAGCGGAGA
12951 AGCATGGCAG AGATGACCGA CAGCTGGGCA GTCTCGGTCA CCGCATCCAA
13001 GTGAGGAAGC CACGGCTTTG CATGGAGGCA GGTCTCCAC ACCAGGACCC
13051 TCACGGGGAA ACAGGCCCAT GGGTAGAATT TGTTCCAAGA TGCTGTCTT
13101 GTCTTAAAGC TCCTTAAAGT TGCCTTTCTG TCCAGCATGC ACTTGCCAAG
13151 TGGCCGGGCA GCTGGGTGAG TGTTTCCGTG TTTGCCTTTG CTTAGCCAGG
13201 AGTGTCTTGC TGCGGTGGGT TTCTGCACCA CAGATTCCAG GGGCCCCCTCC
13251 CTTGCTCACC CAGGCCAATG TCTTGTGTGT TCCCCAAGAG GCCCCCAGGG
13301 CACCAGGCAC TGGGGCATGC TCCATGGATT CTGCCGCTC CAGACCACCC
13351 ACATGGGGCC TGCTGACCCT CATCGCTCAC ACGGTCACCT AATAAGCCTT
13401 ATGCTGTTCT CAGGGCTACC CTGGTGCCCA AAAAGGGTCA GCCACTCTGC
13451 CAGTTTAGGG GAGAAAACCT CTCACCTGTC CAAAGCATAG CTTTGTCTCT
13501 GCCCGGCCCTA CCCAGCTATG AACTGTCTCC TGAGCAGAGA TGAGCACAGG
13551 ACTTTGGGCC CTGGATGCCG GAGAGTGGGT GTTGTGTGA TTCCCCTGCA
13601 GTCTGGAACA GGGCCCCAAG GCAACAGCAT GAAGGCTGTC CAGAGGTCTT
13651 CCATCACCCT CAGCCGATG GGTGTCTGAG CAGTGAGGGA GGGGACCTGG
13701 GAGGGGGGCC CAGCCTGAT CCTGCAGGGG AGAAGAGAAG ACAGCCAGAA
13751 GCCAGCAGCT GTGGCTCAGA TCTGAGCCCG AGCAGCCTCT CGAGGTGGAG
13801 GCAGACACCC CCCACCCAC CCCGTGCAGA AAGAAGCCTT GCCAGCCTGC
13851 CCTGAGGCTG GTACAGAGTC CAGGCAGGCT CAGTGGCCAT CATGCCCTA
13901 CGATGACTGT CACTCCCTCT CCGTGCCTT GGCCTCTGCT GGCTCTGGCC
13951 AGGGGTGGTC ACAGCACTAG GGTGGCAGGG TGGCCTCTGA CTCTGCGCCA
14001 GCCTGCACTG GCCTGTGCTG CCCTGGCCTC TGCTGGCTCT GGCTCTGGCA
14051 CCGGTCCCCT GTTGGCTCCT TCAGCCTTCA CATACCTGCT GCGGCCACCA
14101 CAGGCCCAGG ACCCCCACAG GGTGGCCACC CCACCTCCAC CCCAGGAGCC
14151 CCAGGTATCC AGCTGTACAC CCCTCCCTCC CTCTGGCCT CCCCCTGTCC
14201 TTCTCCAGTT GCCTTCTTTT CCTGCGGGCG CACCACCCAC CTGCCTGCCT
14251 CACCTCTTCC GCCTCAGCCC CCAGGTCCC CGACATCTG AGCTCAGTGA
14301 GGAGGGGCTC GGGAGCCCCA GAAGCCGAGG GGGCCCTGCC CTGCCATCT
14351 CCGGCTCCCT TTAGCCCCCT GCCAGCCCCA TGTAAGTAGC CTGGGTCTTG
14401 CTGCTGTGGG GGTCTGTGTT GAGGGCTGGC AACCCCTAG AGGGGCCACT
14451 CCAGAGCCGA GGGCAGGCTG AGCGTGACC CTGGCTCCAG CCTCATCACC
14501 CCACAATCCC TCACTGGGGC TTTCCAGGGT GGGCCAGCC CATCGAGCCC
14551 CACCTCTTTT TGAGGAGGGC CCTGGACCAC TTTCTGTCTC AAGGCCACTG
14601 GGCAGGATGG GAGCCCTGG AGGCTCGGGC CTCAATTCCA GTCTTCAGGG
14651 TCGGTGCAGG CCTCACTCCA CCTCAGCTTG CGGGCGGGGG GGCTCCCTGC
14701 TATTGAGGCA GGCTCTGATT CAGGGCCTGA TCCCAGGGCC CAAGGGGTCT
14751 AGAACACGGG ACCCCTCCCA CTGGCCTCCT CCGCCTTGCC GCCGCTCGT
14801 GTGTCTGTCT GCCTCATGTT CACGTCTCAT CTGTTCCACC CCAGCCCCCA
14851 GGGATCTCTG ACATCTGAA CTCTGTGAGA AGGGGTTCAG GAACCCAGA
14901 AGCCGAGGGC CCCCTCTCAG CGGGGCCCCC GCCCTGCCTG TCTCCGGCTC
14951 TCCTAGGCCC CCTGTCTCTC CCGTGTAAAGT AGTGGCCCCC AGGCCTGCCG
15001 CCTCTGCTGC CGGACAGCTC CCTGCGAATG GCCGGCGCTC AGCAGCTTCC
15051 CACCTGCATG CACGGCCCAG CTACCCTGCC CCGGCGCCGC AGCCTGGAGT
15101 CCTGCCCTGG CGGGGCTTCC TGTGGGCTCC CATGCTAACC AGCAGGGCAG
15151 CTCTGGCTT CTCCCTAAGG GGCCAGACC CCTCCACGGC TCCTGCTCCC
15201 ACTGCCACTC CCGCTCGCT GTCCAGCCCC AGGCCCTCT CCAAATGTC
15251 TGTCCCAGCC CTGGGCAGCC CTGGCCCTC CGAGGCCCCC CATGCCCTA
15301 GGCCCTCTCT GCTGATCACT GTCCAGCCC CACAGACTTC ACACCCACCC
15351 AGGGGCCCTG CCCATGGTGC CCAGGAGCTG CACTCAGGGC CACCCTGGTT
15401 CCTGATGTGG CCCCACCCC TGAGCACCT CCCTCAGTCT AGGAGGCTGA
15451 GGAAGGTGCC AAAACTGGAA CCCCAGCCAG GGTCTCTGGA GCTCACCAC
15501 AAGGGGATAG TACGGAGAAT CATAAGCCTG GCCTCTGCTG ACCTGGGCTG
15551 TCCTCATGGG GCCAGGCCAG GCCTCCTCTG TAACGCCCGT GACTCCCTCC
15601 TCTCCCTGTA ACCCCGTCCA GCGTTCCTCA AGGGCCACTT ACCTGACAGC
15651 TTCTTGCTGG CCAGCAGCCT CTCCCTGGAG GGTGCCCTCT GCCCCAGCA
15701 GCTTCAGCCC ACGCCACCCG ACAGCCAGAG CATCTGCCCT TCACTCCTGC

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15751 AGCCTCCTCT CCACGCACCA CGCTGTCCGC AGCAGCACCC TCTGTCCCCC
15801 TGTCCTCCCTC CGTCCCCCA TATCCCCCTC GGTCAGCCTA CAACCTCTCC
15851 ACGTCCCCCTT AAGTCCACGC TCTATCCCTA CATCCCCCTC TGTCCCCCAA
15901 ATTCCCCCTCT TTCCCTCAT TCCATTTTCC TCCCCAAACT CTGCTCTGCC
15951 CCTCACATTC TCCCTCTGTC CCCCACACCC TCCTCTGTCC CCCACACCCT
16001 CCTGTGTCCC CCACACCCTC CTCTGTCCCC CATATACCCC TCTGTCCCCC
16051 ACACCCACCT TGGTCCCTTG CACGCCCTTT TCTGTCCCCC ACACCCCTC
16101 TGTTCCCTAC ACTCTCCCTC TGTCCTCCAG ACCCTCCTCT GTCCCCCACA
16151 CTCCCTCTGT CCCCCACACC CCCTGTCCCC CACACTCTCC CTCTGCCCCC
16201 CAGACCCTCC TCTGTCCCTT ACACCTCCCTC TGTCCCCCAT ATCCCCCTCT
16251 GTCCCCCACA CCCTCCTCTG TCCTCCACCC CCTGCCCCC ATACCCCTT
16301 CTGTCCCCCA CACTTCCCTC GTCTTCCACA CCCCCTCCTG TCCCCCACAC
16351 CCCCTCTGTC CCCCAGACTC TCCCTCTGTC CCCCACACTC CGTCTGTCCC
16401 CCACACCTCC TGTCTTCCAC ACCCCCTTCT GTCCCCCACA CCCCCTCTGT
16451 CCCCATACT CTCCTCTGTC CCCCACCTCC CCTCTGTTC CCACACCGCT
16501 TCTGTCCCCC ACACCCCTC TGTCTTCCAC TTCCCTCTG TCCCCACAT
16551 CCCCCTCTGT CCCCCTGACC CTCCTCTGTC CCCTGCACCC TCCTCTGTCC
16601 CATGCACCTC TCTCTGTCCC CCACATCCCC CTCTGTCTC CACACTCCCT
16651 CTGTCCCCCA CATCCACCTT GGTCCCTCA CGCACCCCCA TCCCCCATGA
16701 CCCCTTCTGT CCCCCACACC CCCTCTGTCT TCACACCCCC CCTCTGTCCC
16751 CCACACCCAC CTGCGTCCCC TCATGCCCCC CATCCCTTAC ACCCCCACTT
16801 TGTCCCCCA CATGCCCTC TGTCCCCAC GTTCCCTTCT GTCTCCACG
16851 TCTCTCCCAT TCCCGTTTC CCTCTCTGTC CCCCAGCTC CCCTCCATCC
16901 CCCACATCCC CTTCTTTCCC CTATATCCCC TCTGTGGGCC CAGGTCCACC
16951 ATCTTCCCCC CACACCCCCC CATTCTCCCT TCCTCCCCTC TGTCCCCTTG
17001 TGCCCCATCC CCCACATCTG CCTCTGTGCC CCTCAATCTC TGGCTTGGCT
17051 GTCTGCCCAT GGTTTCTCTC CTGCGTGCCC CCCGTGCTG CCTTGTGTTC
17101 ACGTCTCGTC TGTTCGCCCC CAGCCCCCAG GATCTCTGAC ATCCTGAACT
17151 CTGTGAGGAG GGTCTCAGGG ACCCCAGAAG CCGAGGGGCC CTCGCCAGTG
17201 GGGCCCCCGC CTGCCCCATC TCCGACTATC CCTGGCCCCC TGCCCCACCC
17251 ATGTAAGTAG CACCTTGAGT GGCCGTGGCA GCGGCTGCCT GGAGGGGCTC
17301 GGGGCGTGCG AGCCTGGCAG TGGTGCTCTG GGAAGGGCCA TTCTTGCGGA
17351 GGAGGGCGGG GCACAGGATC CCTCTGCTGG GTCCCAGGGA ATTGCTTTGA
17401 AGCACATGAA GGTGCCACTG GGTCTCAGAA AATGGAGGTT ATGGTTATGA
17451 AGTGTGTATG ACATATGTGT ATAGGAAGAG CGTCCGAAAG AGCAGGTTTG
17501 TTGCCGACCC CAGCATTCGC AACCCTGAGG TCACAGCTT TCTCCTGATG
17551 GGAGGGGAAT GGGTGGCAA GGGTCTGCGC GTGTGGCAAG GGCTAGCACG
17601 CCAGGAGCTG CTGGCTTGGG TCAAGGTGGA CCTGTGCGG CCGGACAGAA
17651 AAGTGTCACT CCCGCTTGA GACGCTCTAG CATTAGAGCT GTCCAAGTCC
17701 AGACAGCAGG GAGCAGGTGG GGATCGGGAG GCGCGGATCT GGGGGGCAGC
17751 TGGGGCCAGG CTGAAACAGA GCGGGCGGGA CAGGAAGCAC AGGCTGGGCA
17801 GCCTCCCCGG CCAGGGAGGA GCCAGGCTGG GCCACCTCCC GGTCTGTCTG
17851 CCGACTACCC GCAGTATCAC TTACAGGGAT GGATGACATC CCAGGGCTGC
17901 TGCCACCCCC ACCTGTGGGG AGACACCAGA CTGGGGGTGG TGTGGAGATA
17951 CTCTTAGAGA AGAGGCTGCT GGGCCACGGG CTCGGCATGG CAGGGCAGTG
18001 GCTAGGTAAG TACTTGAGGG ACAGGTGGGG TCTGCTTGCC ACCGTCCCCCT
18051 CTGCAGGCTG GGCCTGGGG CTGCTGCAGG CGGCCAGGGC AGAAGGTTGT
18101 GGGGAGAGTG AACCACAGG AGCAGCGGCT CGAGGAGGGG GATGCAGGCT
18151 GCAGGCTCAA AGGGGCACTG GATCCACCCT GGGTGCCCGA GAGAGCAGGG
18201 GGCAGCCCCCT GGAGGGGTAC TCACCCCAG AGCTTCTGTG GTCGGCTGAG
18251 GACCCCAAGC AGGGGTTGAC TGAGGGGATC AGAGGCAAGC AGCTGAGGGG
18301 AGAGGCCAGG TTCTTGATGC TGATAGGGTC GGGGTGCTTG GCGCACCAGA
18351 ACTCAAGGAG GGAGGCATGG GGAGGGGCCG CCGTGCAGCT GGGGTGGGTG
18401 CACCGCAGAG CTTCTGGGAG TGGTCAGAAC CCCCAGACCC TGCCACTTCT
18451 ACAGCAGCTC ATCTGATTTT AAGGGGCTTG CTGCCCTTGC AGAAGTGGAG
18501 GGGTGTGCCC AAAGGAGCCT GCCTGGAAGG TCACCCCATC AGGTTGGCAT
18551 GACCCCAAGC CAGGACTGCA GCCTGCCCTC AAGGTCTGTG CAGTATCTGG
18601 GGTGAGTCCT CTGAGGACAG GGCCAGGGT GGGTGTGGAG TGGCCAGCTC
18651 GGGGCTCGGT TTCCAGGCTC ACCTTCAGGG GCCACAGCAC AGACCTGCCC
18701 TTCCAGAGTC TTCCCTGAGC TTGGCTGGGG AGGAGGGGGC TGCAGGAAGG
18751 AGCTGTGAGC AGGGCAGGAT GGAGATTCTG GTGGCCCTCC TGGGAGGGGC
18801 TGGGCAGGGC TGGGAAAGGG GTGGGTGAGA TGTTCGGAA CTCAGGGAAA
18851 GGAAGATCTT GGGTACTGCC CTGGGGGCAC CTGGGCCAG GTGGCAGGTG

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18901 GCCAGCTTTC TGCCTCCTTT CCACCTCCTT TCTCCAGAAG GCACCCACCA
18951 GCTGTGTAAA TAGGGCAGGT GCCCAGGCC CGCCTCAGGC CCCGTCTCCT
19001 CCCACCCAC GCTCTCTAAT CGCGGATTAT ACACAATCCA GCCTGATCCC
19051 TGGGCAGCTG CCTCCCTCC CGCAGCCACC TCTGGCTCTG AGAGATGGGC
19101 TTGGGGCCAG CCTGGGGTCC CAGGAGTCCA GGCCAGGATG AGAACCTGCT
19151 CTGACCCAC CTGGACGCAT TAGGCCTGCC TGGACCTGTT GCCTCACCCC
19201 AAGAGAGCCA CAGGCAATGC AAAGGCTCCT GTTCATGTCA GGGCACCTGG
19251 AAGGCCTGAC TTGCAGAGGC TCTTGGCTCG TGCAGACCCC TCCAAGCCCA
19301 GGCCCTGCCC ACCACCTCCC CTTTGTCTCT GGAAGTCCCA GGACAGCTTG
19351 TCCTCAGCCA GCAGGTTTCC CGACCCGGGC ACCTCTTCAT GTTGGGCCCC
19401 CCTCCTTTCC CTCCATCAGG GATCATGCCC TTCTTCAGGG GCCTGGATAT
19451 CAAGGACACA AAAGCTCCCA TGTGCTATGT GGGGAGGCAG AGTGGGGGCT
19501 GGGTTGAGCT GGGGTCTGGG CAGCGCCATT CCGCAGGGCA GGGGCAGCCT
19551 AGGCTTCCCA TCTGTGGAAT GGGTGGGTGG GTCTCACAAAC GGACCTGCTT
19601 CCCGTACTTC AGCACGGTTA CCACTCTTGA TTGGAAGTCT GACCATGCAT
19651 CTCCTCTTCT GTTTACTTCA CGCTTCTCT TCCCATCAAC TCCCATTTTA
19701 ATTACAATTT GTTTAAAGC ACTGCATATT ACTTCATTAA ACAGAAGATT
19751 AGTTTCACTT ACCATTAGTG TAAGGTGACT ATAGAACCAA AGCAGACTGG
19801 AAACCAAATG ACATAATGTC ATTCTCTTCT CCATTCCAGC TGCCTGCTGC
19851 TGTGCGCCTG AGAACCCCTG TGGAGTGGGA GGGGCAGCTG TCTCTGTACA
19901 TTAGAAAGGG AGGTTAACTA AGTGACAGGA GGTGTTTGGG ACATGTGGAC
19951 ACCAGACTTC TCTCTTGATG CAAGGAGGGC AGAGCCAGGC AGCCTAGTGG
20001 GGGCTGGCTT GGGGGCTGCT GGAAGGACTG GCTACAGGTG GAAGAGAGGT
20051 CAGACCTGAA GCTTGGGGCC ACCTCCAGGA AAGGACAGGT GAAAGTGGAG
20101 GCATGAGGCA GGGGAGAGGC AGGTGCCAGG CAGAGGGTGG AGAGGAGGCA
20151 GGAACATAGC AGCTGGGGCG GGGGCGGGCC CTCAAGTGTC ATATGCTACT
20201 TTCTTGGGGC CCAGGGGCAA GGACAGGAAC AGCCACAGCA TGTGTTGGGA
20251 CAGAGCCCTG TGCCTTCCTA GAGCTGGGCA GGTGGAATGG GGCAGGAATG
20301 GGACTCGTGG TGGCTGCAGC AGGAACTGGA GGGGAAGGGG CTTCTGGATC
20351 CTGCAGCCTA CCTTCCTAGA GGCCAGCTTT CCGGGGTCCA CCAGGTGGGT
20401 GGGAAGTGGG CTTGTGTAGC AAGACTGCCC TGAGGACCAT CCATGACATG
20451 GTCTAGATGA AAGTTAGGAA AGAAAGGGAG ACAAGCTGGC AGCAGAAGTA
20501 CAGCTGGGTC AGGAGCAAGG GCCTTTCCAG ATAGGGACAA CCCAAGAGTG
20551 CACATGTGCC CACGCCACAC AACACAGGCA CACACGACAC GTGCACGCTC
20601 ATAGGCACTG CACACACACA TGCACAGGTG CTATGCATA TGTATGAGCT
20651 TCATCTACAC ACATTACAT GCCGTCTGTC TTATGTGCAT GTTTCCATAC
20701 ATGCACATGA ATGCACAATC ACGTGTACAC ACATGCATGT GATCACATAC
20751 ATGAACATGT GTGCACCCCA CTCCTCAGGT GCCATCGGGC TCCTCCTGCT
20801 GTCACTGTGC AGCAGGGGAC ATGAGGCCCC AGAGCAGACA GGTGCAGCAC
20851 AGGCGTTCCC AGGCAGTGCC CCACACACAT GCATGAGCAC ACCCGGGCAT
20901 GTGGCGCCTC CTTTGTGGAC TCAGTCCACC TGCCAGGTGG GCTCCCTGGT
20951 GGTGTGAGCT CCCAGAGGTC TGGCGAGAGA GATAAAGGCA ACCCCACCAC
21001 CAGGCGTGCT GAGAAATCCC TCTTCTGGCT GGGCACAGTG GCTCATACCT
21051 GTAATCCCAG CACTTTGGGA GGCCGAGGTG GGCAGATCAC TTGAGGTTAG
21101 GAGTTTGAGA CCAGCCTGGC CAATATGGTG AAACCTCATC TCCACTAAAA
21151 ATATACACAC AAAAAAATTA GCTGGGTGTG GTGGTGTGCA CCTGTAGTTC
21201 CAGCTACTCG GGAGGCTGAG GCAGGAGAAT CGCTTGAACC TGGGAGTCAG
21251 AGACTGCAGT GAGCCGAGAT CATGTCACTG CACTCCAGCC CGGGTGACAG
21301 AGTGAGACTC CATCTAAAAA AAAAAAGAA TTCCCTCCTC TGGGAATTTA
21351 GACCACAGAC AGGTTGCATG TATGTGGCCG TTGGAGGCAG CACTCACAGC
21401 AAAGAGTGGA AACGTACCA CAGGGCCTGC CTCTCGGTGA AAATGGTGTC
21451 CTGCAGGGCG GGCAGCTGTT TGAGGGCAGG TGTCACAGGT GCGGCCTGCA
21501 GCAGCCTGAG GGTCAACAGG CGCAGTGCTG GGAGTGCAGA GACTTCCCCC
21551 ACAGGGAGAG TTTCCAGGAA CCTGCTTCCG GTGCACTTCT GGGGGTTTGA
21601 GTTTTTTCCA CGGACGAATT ACTTTGAGAA ACCACTGTTA CTCGTGTGTA
21651 TAGGTGAGCG TGCGTGTGCA TGTGTGTTCT GTGTGTGAGT GTGCATGTAT
21701 GTGCGTGCCT GCGTATATAT CCTCGCAGAT ACGGCTAGGG ACCTCACTCA
21751 GGACAGTAGT TCTGCCTGAG GAGAGTGAAT GCGGCAAGAT TGAGGAGAAC
21801 ACAGGCATCT TCAAAGTACA TGTGCGGTGC TTTATTTCTT TAAAAATGCG
21851 TCTAAAGCAA ATAGGAAAAT GTTAAGATTT GAATCCGTAG AGTGTGGGTT
21901 CTATTATTCT TCCACATCT TCCATACGTT TAAATCTTT TGCAATGAAA
21951 ATAAGCTGTA GTTAAAGCAG CAATGCAGGC TGCCAGTGAG CGCCCCGGAG
22001 GCCAGTGAGG ACCAGCATGG CTGGGTGGCC TGTGGAATC CAAGGGGGGC

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FIGURE 3, page 7 of 16

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22051 GGGCAGGAGC TGCAGGCAGG CGCCCGGGAG TAGCCCGGGC ATGGGGGTGC
22101 GGGGCAACAG GGATGTCTGC AGGGGTAGCA TGTGGGCCCC GGAAGCAAG
22151 CAGGTGGAGC CAGCCGATG CGGCTCCTAT GAGAAAAGCG GGAACAAGA
22201 GACCACGCTC GTTCTTCCTG CTGCGGGGAC AGCCCTGGTC ATCGCTCCGG
22251 GGAACCTGCT AGCCTGCGCC GCACGTGGCC GCCCCCTGCT GCTTCTCCT
22301 CCCC GGCCCTC CGGGTGGCCT TGCTGACGGC TCCTTCTCTG AGGCAGGTCT
22351 CTGCTTCTC GCCTGGTGCC TGCACTCAGT AGCCCCCTCA CCAGAGCTGC
22401 TGGGTGAAGG AAGCACTAAG AACCAAGGC TCGGGAGGAG AGTGGGGCCG
22451 GGAAGCTGCA GGAAGCGCA GGGCCAGGCC TGGTGGGCCC AGGGGCTGGC
22501 TCACGGGAGG GCAGGAGGGA GACTGTGGCG GACAGCACGT GGGGCCAGGA
22551 GGTGACCTCC AAGTGGATTG TGGGTGGGTT TTTTGTCTC TTTCTGCATT
22601 TTCCAGGCAT TTTGTAATGT GGATAGAATA TTTCTGTTCT TCAAAAATAC
22651 TTTAGTTAAG AAAAATAAGA TGGAAGCTGT TGCACTTGAA AATGAGGAAG
22701 CCACTGGTGA TGCAGGGGGG GCGGCGGAGA GGACCTCTTC TGCAAATAGC
22751 GGCAGGAACA CGGCATGGAT GCAGCTCGCG CTCCCCCAGG CCCTCCCCTG
22801 GGCTGTGTGG AGGGGTCCGG GGGGAATGGG CCAGCGCCCA GTGGTCACTT
22851 TCACGGGTCT CCCCACAGCC CGGAAGCAGG AGATCATTAA GACCACGGAG
22901 CAGCTCATCG AGGCCGTCAA CAACGGTGAC TTTGAGGCCT ACGCGTGAGT
22951 CCCTGGGGCT GGGGGGGGGC TGTGCAGGAC AAGGATGTGG GACCCTTGGG
23001 GGGGCTTGCT CAGAGTCAGG GGTCCACGGG GCCCTCCTC ACTTGATTTT
23051 GGCCCCCAGG AAAATCTGTG ACCCAGGGCT GACCTCGTTT GAGCCTGAAG
23101 CACTGGGCAA CCTGGTTGAA GGGATGGACT TCCACAGATT CTACTTCGAG
23151 AACCGTGAGT GAGCAAGCCC GGTGGGCAT GAGGGGGCGG TGCCCCCAGG
23201 AGAGCCTCTC GGCCCCTCCC AGGGACAGCA TGGTGGCTGC CTATGGAAGC
23251 CCTGTCCCCT CTGTGCCCAG GGTGGCCAG CCACCTCTCC CCCGCCAGAG
23301 GCCATACCCA GCCCCCAGAA TCCCCTCTT GGAGGGGGCC ATGCTGCTCC
23351 CAGGAGAGCC GAGCCTCCCC AATAAGGGGA GTTGAGAGAG GGAAAGGATT
23401 AGGCTGGTGG GGTGGAAGAC GGGCACCAGG GCAGTCATGG TAACCCGAGA
23451 CCCCCGCCCC ATCCTGTGTC CACAGTGTG GCCAAGAACA GCAAGCCGAT
23501 CCACACGACC GCCTGAAACC CACACGTGCA CGTCATTGGA GAGGATGCCG
23551 CCTGCATCGC TTACATCCGG CTCACGCAGT ACATTGACGG GCAGGGCCGG
23601 CCCGACCA GCCAGTCTGA GGAGACCCGC GTGTGGCACC GCCGCGACGG
23651 CAAGTGGCAG AACGTGCACT TCCACTGCTC GGGCGCGCCT GTGGCCCCGC
23701 TGCACTGAAG GTGAGTGTTC TGTGCTAAGT GACAGCTGGG GCAGAGGGGT
23751 GGGGTGGTGG TGAGTGGCTG CAGCCTGGGG AGGCGATGGG GAGCGTGGG
23801 GCCTGTGGCA GAGCCCATGC CTGGGAAGTC CCTGAGCTTT CCTGGTGAGG
23851 CCACAGGAAT GATGTCAAAT TAGGGACCAC GGCAGGCTGG GTGTGGCAGG
23901 CCTCCCCAGA GGAAGTGGGA GCTGTGAGG GCCTGAGCAG TCCACACTGG
23951 CCAGAGCTGG GTGGGTGCA GGTGGATGGG CCCC GGCGAG CACAGTCTTG
24001 GGCACCATGC CCTGTTTGTG AGGACTGTTA GAGCCCCAGA TGGGCGTTCC
24051 CCAGGTGGTG GGTGCAGCGG GCCCAGAGCC CAGTTTTACA GGGATAGTAG
24101 TAATTGGGTT GGGCACCTTG AACCTCTCTC CCGAGTGGGC CCTTTTCTGG
24151 ACTTTAACCC TCTCTGCAGT GCCGCATGGC AGACAGCAGA GCCTGGGGGT
24201 GGATGGGAGA GGGGGCTGCT GAGGAGCTGA CCCACCCGCC CCATTTCAAG
24251 GCTGCGCCCT GGTTCGCGG GACAGAGTTG GTGTTTGGAG CCCGACTGCC
24301 CTCGGGCACA CGGCCTGCCT GTCGCATGTT TGTGTCTGCC TCGTTCCCTC
24351 CCTGGTGCC TGTGTCTGCA GAAAAACAAG ACCAGATGTG ATTTGTTAA
24401 AAAAAA AAAAAA AAAAAACAAG ATGACGACGA CAACCACAAA
24451 AAAAATTGAC ATCAGATGAA ATGAAAAA AAAAAACAA AAAAAACTAA
24501 AGGAAGGAAA AAGCTGTAAA AATCACTGGC ATTCGTGGGG CCACTCCCCA
24551 CCCAAGCTCC ACGTGTGTCC GTCTGTGCTC CTGGCCTCTG GGGGACCAAG
24601 TGGGACATGA ACTTGTCTGC CAGGCCCCCG TCGCGTGTG AACGGTGTTA
24651 GTTTGTAGGT AACGCACACA CCCCACACCT AAGGTGTCTG CATCCTCTG
24701 CCAACGCATG GGCTCCACGT GGTGTGCTCG CTGGCTGTG TGACTGTCAG
24751 CTGTCTCTTG GGAGG3GCTG TGGGGGCCCC CTGGGCTGCC TCCTTTCCCG
24801 CTAGTTGTGC CTGAGAGTTG CTGTTGTTCC TGCTTTCCCT TCCCTTCCTT
24851 TCATCCCCCTG AAGGGCTAGG TGTGGGTTTT CCGTGCCCGG TATCCCCACA
24901 CACCCAGCAC GGACAACCTT TCGGCAGAGC CCAGGCCGGC CCCTCACCCC
24951 CTGGAGTATT GAAACTGGAG TCCCGTCCCC AAGGCCTTCA GAGATGCCCC
25001 TACACACCCA GGGCTCCAGC TCTGTTCTTT CTGGGGGAGT AAAGTGCAAA
25051 GAGGGGCACA GCTTAGTTTT GGGCCTCTCG CCGAGCAAGA GACAGCACTG
25101 CTGGCTACAG CTCCAACACA GCCAGCTGTG GCAAGAGGAC TCTGCCTGGG
25151 CTGGCCCCC TCCTGTGTGA GGTGTCTGTC CCTTCTCTGC TGGCCAGCAG

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25201 CAGATGCACT GGCAGCTCCC AACCTGTTT CCGCCCCTCG GCCCTCCCCC
25251 AGCCTGTTTC GCTTCTCTGC AGCCCGCAAG GGGGAGCAGA CTTTGTGACAA
25301 AGGACTGCGG GCCTCGCTCA AGTCCCTGAG CCCCAGCTG AAGCTGGGAG
25351 GGGAGGCCAG GCTTTGTGTC TGGGCATATT CGTCTGCTGA TGGGGTTTGG
25401 GGAAGCCTGG GGCTTGGGGT TTGGTCGGGT GGTGCAGCTA GTGGCAGAGC
25451 GGGATCAGAG GTGGTGGCTG CCCAGCTTCT GGGCTGAGAC AAGGGTCTGT
25501 GCAGGGGTTT ACTGAAGTGG GAGTGCTTT GGAATCTGGG CCGGGAGCAG
25551 AAGGGAGCAA AAGCTACAGT GGGAGCCAGC CTAGGGCACA TGGGAGGCGT
25601 GAGGGCAGTG CTGCCCCGTC AGTGTCTAGT GTGCCAGTGC CTTGGCGGGC
25651 TGCAGTGCGT GTGAGGGCAC CTTCTAGGTG GGCCAGGGAT GCAGCTATGG
25701 AGATAAGGCG GGCTGGGGAC AGAAACAGGT GGGCACAGGG CCCAGGACAC
25751 CAGCGGATGG AGGGCAGGGT CTAGCCCTGT GCTCCTGAGC GTCGGCTCC
25801 TGGGTTTCGAG GCGGTGGGTC CCCGGCCCCC TGTGATGGTG TGTACCATGG
25851 GGGAGCTCGG GGACAGGGCA AGCCCGAGCA TGGTGGGGCT GCAGGGTGGG
25901 TCTGAAGCCA GGTGGGGTGG GGGTGGTCAC AAGCCCTGAC TGCAGAGGGT
25951 CAGGGGCTCT TGCCCCAGTG CCTGCCCACT TTCAATTAC ATTGTTTCA
26001 ACAAGGATTT TCTTTATCTT CCCCTACAAA TCAAGCCAAG GGAGGGGCAC
26051 AGAATGGGGA ACAGGACACA GGATCCTAAA CTCCAAGGGG ACTGTCCACC
26101 GATGAACACT CAGAGTGGAC ACCATCTTCC GTCCACGCTG TGCCAGGAC
26151 AGCTGTCCCC ATCCATGAAC ACAGGGTAAA CATCTGCCCG GCTCCGCACC
26201 AGTGGCTCCC TGGGCCATGG GACAGCGGCA GGGCTCACCA CGGACAGCAC
26251 GTGGCCCAGC AGCCGGCCAC CCTGGCGTCC TGGGGCTCC TCCCCCTCTC
26301 TCCCTCTCAC CTTGTCACTT CCACGAGCT GCCTGTCTGG GATAATTGG
26351 GGATTTTTTT TCTGGGGGAT AATTCTTTTG CATGACCCCT AAAGAGCAAG
26401 CCACACCGGT CTGCTAGCTA GGTGTCCGCG GTGTGGTGGT GCGGGCCGCT
26451 GGCCAGCGCT GCAAGGGGTC GGCTGCCAC GGTGCTGGCT GGCCTCCCT
26501 CCTCTCTCTT TTGCTGAGT TTCATTGTCT TTTCTTTCTG AGCCTTGTA
26551 GTGTACAAAA ATTATTCTTA TTTTGTCTG TCTCGGAAA CTGCAATAA
26601 AAGAAAAACA GGACAAACTG CTTCAAGTGC AGCTGGGTGC TTTAGCTGGA
26651 ATCCTGCCGA CCTCCTGCGC CAAAATACAG ACTCAAGCCC GGTCCCTGGC
26701 CAAGACCTTA CTTGGGCCCC TCCTCCAATG AAAGGTAGTG CTATGGGAGC
26751 CCTGAGCTGG CCTGACAGT CCTGAGCCCC TCTAGGGTGA ACGGCTCACC
26801 CCAGGTAGGG CACTAGTCAT AGATCATAGC TCTACCAGCT GTCTCCACCT
26851 CTTCTCTGTT TCCTCTGAAG TCTTCTGGG CCAGCGCTGT CCACCTGAA
26901 TGCTGGAACT GAAACTGGAT CCCAGCCCC AACACCCCTG ACCTCTCCAT
26951 TCACCCCCGG TGGCCGCTAA GGATGTGGCC AGGGCAGCCT CTGGGCAGGA
27001 AGGAGCCCCA GGACCAAGAC CTCTGGCTGT CCTGCTGTTT CTTCCGCCC
27051 CTGCTACATG TATTGGCTAT TCTGGATGCT GAGGACACAC AGTGACCACA
27101 GAGCCGGGCT CCACCCAGT GGATTATGCA GACAGATGGC ACGCAGGCCT
27151 GTGTGGACAT CAGCCTCGGG CACCAGACAT AGGCAAGGCG CAAGGTGATA
27201 CAGTAGGCAG CAACCATGGG GGCCAGGAGG CTCCAGCAGA GGCCACACAA
27251 CCAGCCAGGA ATCCAGGACA GAGAGCTGGA ATGGAGACAG GGAAGCCAGA
27301 TACCAGGCCA GACTGGCCAG GTGCTACAGG CCTGTGGGCC AGGCCAGGCT
27351 TGGGGACTTC GTCTGGGTG TGAAGGAGAC AGGCACCCCT GAGGCCTTCC
27401 CTCTGCATCT CCAGCCCAAG CTAAGCGCAA ACTCTTAGGT TGGAGTAAGG
27451 AGTAACCCCC TGCCAAGTTT CTCTGTCTCT CAGGCTCCAC CCACCACCTA
27501 TGCTGCCTGG CCCCATGGGG CACACGCTCA GGCCAGCCCT GGGAAAGCAA
27551 CTGCACCTGC CTGTGCTATG CTGGCCCTTC TCAGCCTCAA TGCCCTCCTC
27601 CCTCCCCGAC GCACCTCTGT GGCCCCGCT GGGCCCCCTG ATGCACCCTC
27651 ATGTCTCCAT GGCAACCTGC TCAGAGTGTG GCCTTGCCCT TGGCTCCCT
27701 CCACACCTGT GTCCAGGCA GTGCCACGGC ACTTCTCTAA ACAGAAGGAT
27751 GGGCTTCAA ACAGTCCCAG ACCTAAACA CACCTGCATT TTGGGTCCAA
27801 GTAACCTCTG ACAAGACGAG TGCCCCTACA CACCTCAGT CCTATCCACT
27851 ATGGGCAAGG AGCCTGAAGG ATCCCCCAGA ACTGGCTAAA GCCCTCAGTC
27901 TCCTCTCCA CCCTGAGCAC CTTACGCGG CAGAGTGGCC CTGGATGTCA
27951 GCTTCTTGCT CCCCATGGTC TGACCTGGA CAGGTGCTCT CAGGTGTGTG
28001 GGTGGGCAGG TGGCAGGTCC CAAGAGCCAG GTGCAAAGAA TCTAGGCCAG
28051 TGCCCACGAG TGCTGCACTG TCTGTCCCCA GCATGGTATC TAGGGCTCCA
28101 CTTGCCTATC AGCTGTAATC GGAGGAGGCT TTCCAGGCCA GGCCTCCCCC
28151 AGGAAGGCTG CAGGCACCTG GGATCGTGCG CCTCACATG CATTATTCTC
28201 GAGGCCCTTC TGCAGATGCC ATCAGGGCAG CAACTCTGAT GAGGTATTAG
28251 GGCACAGCAC ACAGGGCTAA GCCACCTGT ACTGGCCAA GCGCTACAGG
28301 CAAAAAGGAC ACCACCGACG GGCATTTTAT TCATCGCTTT TATTTTTATA

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28351 TATTTTGTAG AGGGAGCCTC ACTCTGTCGC CCAGGCTGGA GTGCAGTGGC
28401 GCGATCTTGG CTCACTGCAA CTTCTCCCTC CTGGGTTC (SEQ ID NO:3)

FEATURES:

Exon: 232-340
Intron: 341-431
Exon: 432-515
Intron: 516-1110
Exon: 1111-1205
Intron: 1206-1424
Exon: 1425-1547
Intron: 1548-1981
Exon: 1982-2065
Intron: 2066-3015
Exon: 3016-3058
Intron: 3059-4102
Exon: 4103-4177
Intron: 4178-9088
Exon: 9089-9126
Intron: 9127-9303
Exon: 9304-9375
Intron: 9376-10898
Exon: 10899-10943
Intron: 10944-12713
Exon: 12714-12762
Intron: 12763-17130
Exon: 17131-17133
Intron: 17134-22868
Exon: 22869-22944
Intron: 22945-23137
Exon: 23138-23154
Intron: 23155-23475
Exon: 23476-23705
Stop: 23706

CHROMOSOME MAP POSITION:

Chromosome 7

ALLELIC VARIANTS (SNPs):

DNA				Protein		
Position	Major	Minor	Domain	Position	Major	Minor
487	T	C	Exon	55	H	H
496	T	C	Exon	58	L	L
1662	T	C	Intron			
1785	T	A	Intron			
1889	A	T	Intron			
2416	C	T	Intron			
4698	A	G	Intron			
5424	C	T	Intron			
8722	C	A	Intron			
9982	G	A	Intron			
10951	C	T	Intron			
12603	T	C	Intron			
14583	C	T	Intron			
17290	T	C	Intron			
18188	C	T	Intron			
19911	A	G	Intron			
21328	C	A G	Intron			
21391	T	C	Intron			
22588	C	T	Intron			

22965	-	G	Intron			
23498	G	A	Exon	312	R	R
23663	T	C	Exon	367	S	S
25427	A	G	Beyond ORF (3')			
27727	C	T	Beyond ORF (3')			
27834	T	C	Beyond ORF (3')			
28336	G	A	Beyond ORF (3')			

Context:

DNA

Position

487	CACCTCTGGGTTTAAACAACATGCACCCTTGTGCCGGTCACCTCCCTGCAGCCGGAGAAC CTGCTTCTGGCCAGCAAGTGCAAAGGGGCTGCAGTGAAGCTGGCAGACTTCGGCCTAGCT ATCGAGGTGCAGGGGACCAGCAGGCATGGTTTGGTGAGTGCCAGGGGCAGGGTGTGTTG GCTGGCAGTTGGCAGGGCAGGAGGTGATGCTGACAGCCCCTTGTGGCCTCTTCCCCTCTC TCTAGGTTTTCGCTGGCACACCAGGCTACCTGTCCCCTGAGGTCCTTCGCAAAGAGGCGTA [T, C] GGCAAGCCTGTGGACATCTGGGCATGTGGTGAGGCCTGGCCTGAGTTGGTGCGGGGCAGG GCCTCGGGTGTTTTCAGGACTTCCACCTACATCCTGGAGTGTGCAGTGGCCAGCACGTCT TGCTCTCATCTGGGTTTATCTGTGTGACACCTGCCCTTGAGCTGCCCTGGCAGGGGTCTG CCCACACAGCCAAGAGCCCCCTTCCACCCAGATTAGAATTGCTCACATGAACCTGGCGC ACCCAGTGCTCGCCTGCGCTCAGCAGAGGTCTGGTCCAGAAGTGTGGTGGGTGGATGGG
496	GTTTAAACAACATGCACCCTTGTGCCGGTCACCTCCCTGCAGCCGGAGAACCTGCTTCTG GCCAGCAAGTGCAAAGGGGCTGCAGTGAAGCTGGCAGACTTCGGCCTAGCTATCGAGGTG CAGGGGACCAGCAGGCATGGTTTGGTGAGTGCCAGGGGCAGGGTGTGTTGGCTGGCAGT TGGCAGGGCAGGAGGTGATGCTGACAGCCCCTTGTGGCCTCTTCCCCTCTCTCTAGGTTT CGCTGGCACACCAGGCTACCTGTCCCCTGAGGTCCTTCGCAAAGAGGCGTATGGCAAGCC [T, C] GTGGACATCTGGGCATGTGGTGAGGCCTGGCCTGAGTTGGTGCGGGGCAGGGCCTCGGGT GTTTCAGGACTTCCACCTACATCCTGGAGTGTGCAGTGGCCAGCACGTCTTGCTCTCAT CTGGGTTTATCTGTGTGACACCTGCCCTTGAGCTGCCCTGGCAGGGGTCTGCCACACAG CCAAGAGCCCCCTTCCACCCAGATTAGAATTGCTCACATGAACCTGGCGCACCCAGTG CTCGCCTGCGCTCAGCAGAGGTCTGGTCCAGAAGTGTGGTGGGTGGATGGGAGTGGAGAA
1662	GAATTCTTGCCCCTGCCCTGAGAGGGAGCTTCAGGCCCCGGCCGGGGCGCTGTTTCTTCTG CAGTTCCCGTCCCCTGAGTGGGACACCGTCACTCCTGAAGCCAAAACCTCATCAACCAG ATGCTGACCATCAACCCTGCCAAGCGCATCACAGCCCATGAGGCCCTGAAGCACCCGTGG GTCTGCGTGAGTGGCCCTTGGTGCCCATGGTGGGGAGGGGGCTCCTGGTGGAGATGGCCT CAGACCACTCCCCTGGCAAGGACCCCAAGAGGGTCCTGTTCTGACATCCAAGAGCTCCC [T, C] TGGGTCCCCTGGGTGCTCCTTGTGGCCTCTGGCTTGGGACATACCAGCACGTTTGTGAGG CCTGGGGCTTGGAAGGCATTAGAGGGTAGAGGTGATCCCTTCTCCCAACTGCAGTCCTG TCTGTGAGGGGCAGAGTGGACGAGGCAAGGAGAGACGAGTCTTGAAGTCCCAGGCGGGT GGGGACAGACAACCTTGCCGCAATGGTGGCCGGTGGCTCTTGGCAAGTGGGGACCCAG GGTGCCACAAGCCTTGCCACCCTGGCCTCTCCCCTGTGCCTCGGGCTCGGCTGCCATATG
1785	CTGACCATCAACCCTGCCAAGCGCATCACAGCCCATGAGGCCCTGAAGCACCCGTGGGTG TGCGTGAGTCGCCCTTGGTGCCCATGGTGGGGAGGGGGCTCCTGGTGGAGATGGCCTCAG ACCAC'TCCCCTGGCAAGGACCCCAAGAGGGTCCTGTTCTCTGACATCCAAGAGCTCCCCTG GGTCCCCTGGGTGCTCCTTGTGGCCTCTGGCTTGGGACATACCAGCACGTTTGTGAGGCC TGGGGCTTGGAAGGCATTAGAGGGTAGAGGTGATCCCTTCTCCCAACTGCAGTCCTGTG [T, A] GTGAGGGGCAGAGTGGACGAGGCAAGGGAGAGACGAGTCTTGAAGTCCCAGGCGGGTGGG GACAGACAACCCCTTGCCGCAATGGTGGCCGGTGGCTCTTGGCAAGTGGGGACCCAGGGT GCCACAAGCCTTGCCACCCTGGCCTCTCCCCTGTGCCTCGGGCTCGGCTGCCATATGACC ACCATTTCCCCACAGCAACGCTCCACGGTAGCATCCATGATGCACAGACAGGAGACTGT GGAGTGTCTGAAAAAGTTCAATGCCAGGAGAAAGCTCAAGGTGAGGCCCTGGCCCCTAGT
1889	GTGGAGATGGCCTCAGACCACTCCCCTGGCAAGGACCCCAAGAGGGTCCTGTTCTTGACA TCCAAGAGCTCCCTTGGGTCCCCTGGGTGCTCCTTGTGGCCTCTGGCTTGGGACATACCA GCACGTTTGTGAGGCTGGGGCTTGGAAGGCATTAGAGGGTAGAGGTGATCCCTTCTCTC

FIGURE 3, page 11 of 16

CAACTGCAGTCCTGTCTGTGAGGGGCAGAGTGGACGAGGCAAGGGAGAGACGAGTCTTGA
AGTCCCAGGCGGGTGGGGACAGACAACCCTTGCCGCAATGGTGGCCGGTGGCTCTTGGCA
[A, T]
GTGGGGACCCAGGGTGCCACAAGCCTTGCCACCCTGGCCTCTCCCTGTGCTCGGGCT
CGGCTGCCATATGACCACCATTTCCCCACAGCAACGCTCCACGGTAGCATCCATGATGC
ACAGACAGGAGACTGTGGAGTGTCTGAAAAGTTCAATGCCAGGAGAAAGCTCAAGGTGA
GGCCCTGGCCCCCTAGTCCCAGGCACGGCCATGCTTCTCTGTGTCCCTCTGGGCTGGAGCA
GGGGGGCCTTGGGGGGTCTGGGCAGACCTAGGGGTTACTGCTGCCCCAAGACTGACTGT

2416 TCTGGGCTGGAGCAGGGGGGCTTGGGGGGTCTGGGCAGACCTAGGGGTTACTGCTGCCC
CCAAGACTGACTGTAGCAAGTCCCAGACTGGATGCATCAGGTGAACCTCAGGCCAGCTTG
GGAATGAGTCCAGAGGGGGCCTGGGCCAGGTGTGGCTCCTCTAGTTGTCTGTGCCACCT
CCTAGCAGCCCTTGAGGAGTGTCTGAAAGCGCTCGCTGTGGGCTCCTCACCCGGGCTC
TGCAGGCAGCACTCACCCCTCTGGCAGTCACACTGTTTAGTACAAGCAAGTCCGAAGCTTC
[C, T]
GGCTCAGACAGGTTTGGAAGGAGAGCAGAGCCACACACACTGGTCTTGGGTGGGCTGGG
GGAGTTCTGGGAGGGAGGTGGGTCCAGTAGGGTATCCAACCTGCCTGCTTTGGTCAGGG
CTGGCTCCGGTGACCGCACACTGGCAGTCCCTCTACTTGTGGGTTCGGGATGGGACTT
GTTGCCTGACTGCCCTCTGTGGTCTCTGAGCAGTTCTCCCGAAGCCCCAGGACTGTT
GCCCTGTCTGAGCCTGTGAGGAAAAGAGGGGCTGTGAGGGAGCTGGACCCAGAGGAGC

4698 GCTAGGTGGCCCCCTGGGCTACACCAAGCCCTTCTGGTCTGGCCCCGAGGTCTGGGGGT
CCGGAGACCCCCATTAAGAATGGCCTGGGGCCCCACAGGGAGCCACTGGGCCTGCTGCTGG
GGGTCTGAATCCTGAAAGGAGAGCCTTGAGGAGCAGAGCCAGAGAGGCAGAGGCCCTTG
GGGCAGACACACCCCTGCCCTCTGGGGCCGATGGAGACGGTGGTCTGTGCTGCTGAG
TCCTACACATGCATGTCTGCCCTGAGCATCCCCCAGGACAAGCCGCTCTGGAGTGGGTG
[A, G]
GGGTTTTATGCACCCCTGAGGAGACTTTCAAGGCTTCCTCTTGGGTGTTTCTGCAAAGTC
CTCCTCCCCCTGGCCTCAAACCCTGTGAGGGAAAAGGCCGGCACTGGCCACCTGCTCCTCT
GGGCTGTGCGGGGCCAGAGCCCAGAGGCCCAAGTTGGCTTCTGCCACCTGCTGGCTTGT
GACCAT

5424 CCTCCTCATGACCCACAGGGTGAGCAGCCTGGCCTTCCCAGCCAGAGAACCCTCCTTCTG
GGGAGGCCCAGGGCGTCTCGGGGAGGGCAGTCTATTCTCCTCCCATGAGCCAGTGGAC
GTGTCTAGCAGGCAGCACCCCGGGAGAGCCCTCCACGCTCTTCTCCATTGACAGGCCTT
TCCAGAGCGCAGGCGGGAGGGGGCTGTGATTAGAAAAGAGTGAGGCTAGTGGCTTCTGGG
GAGGCACTGCTGCCAGGGGACAGTGTGAGAGACAGCTGCCTCTACGCTGCCCTGTGCC
[C, T]
GGGGTCCCCTGCAATGCCCGCCTGTCTGCAAGTGAACGTGGGGCGACGGTGATGAGG
CCCTGCATGTGTGGCTCCACCCTGGGCGCCGAGAGCAGCTCTGTCTGGAGGGTGGTCAG
TGCATGTGGACAGAGCCACAGCATGGCTGTCTGGGTGACCAGCTAAGGGGACAAAGGCAGA
GGCAGGGCTGAGAGGACACCCATCCTGCTAGGTGAGCCAGCTCAGCCATATCACACGG
CAGTGAGCATGGAGCTCAGTTCTCTGCCAATGGCAGCTGAGTCTAGTACCATCCAGTCAG

8722 AAGGCCTGTGCTGGCCCCAGTCAGTGACAGAAGCGGCCCAAGGCCAGGGCTGCTGGGC
AGCTCGGAATGAGGGCGAGCAGGGCTGCCCTTGGTGCCTGAGCCAAGGAGCCAATGGGAC
AGACCTCTGAGCCTGGGTGCCAAGTATGAGGTCTGAGACAGGGTGAGCGCCTGGGCTGGG
ACAAGGCCCTCTGAGTGGGCGGCCAGCTGCAGCCACCCACCCCTACCCAGGAAGGCAG
GGCCCGGGAGGGCATGACCTCTGGGGTGTGGCTCAGCTGCCCCCACCACCACTGACAC
[C, A]
GCTAGTCCCTGAGTTCCCATCAGGGAGGAAGCAGCATCCTGCCTTCTCTAGGAAGAGCTT
GCATGTGGCCCAGAAGCCAAGGGGGCTCCCCAGCACCCACGGGCATCTCTGGGTCTGGTC
AGAGGAGAAAATCTGGATGCTTGCAAGGAGCCCAAGGTGATGGAGGAGGCTGGAGACAGGG
CTGTCTTGGGGTGATGGGATGGCCCCCACCCTGCTCAGAGCCAGCCTGGGTGCTGGAAC
CACACTTGCCCTCAGGACCCTGGGCTTGCTCCTGGGGAAGAGTGGGGTCAGGCAAAGGGG

9982 CCAGGAGTGTTTCAAGGAAGTCAGTGAGGCAGAAGATACCCTCTCCCCACCAGGACCCACC
CTCAGCTCCTCCACCATCCTCAACAGGCCGACCCACAGACCACTCCGAAGGTCTGGCTTG
GTGGGGCTGGGCCAGGATCTGCAGGGGGAACAGCCCATAGTGGCACATTCCACGGCCCAT
GGGGAGACGGGGCCACGGTGGTGACAGTAGAGAGGTGTCTAAGCCAGTGGCAGCCAAAGGG
AGGGCTTGCCGTACCTCTGTGTCCCTCAGTGTCTGTGGCTGCCTGAGAGGCAGG
[G, A]
CTTAGGGGCTCCCTGCCGGGGAGGGGAGGGGTCCCCACCATGCTCCGCTCCAACCTGCGCC

FIGURE 3, page 12 of 16

CCTCAGTGCCCCCTTGCCCTGGGGGCTCCTACAGGTGAACCTATAGCAGTACTCCCAAGG
ATGTAAGATTGTGGCTGGTGGGTGCCGGCCTTCTGTGGGGCGCTGTGCTGTGTCCCCT
CAGCTGTCCTAAGAGCTTTGGGGCTTGCTGGCCCGTAGGTCCCCATATTTGCTGGAAGCA
GGCTTGGTGTCCCCTGAGAACCCAGGCCAGGCTTCGGGAGCCAGCCCCAGACCGCCAC

10951 ACAGCAGCACCTCCGCCAGCCTGGACAGAGCTCCTGTCCATTCCATCCCTGCCGGCTGAC
CCAGGTCCTCCCCAGCTGTCACGCCGCTCCATCCCTGTCCCCCACTCTGCTCTGC
ACTTCTTTCTCGCAGGCTCTGGCCACCCACACCTCCTCTGTCTCCCTGTTCCCTCCTGG
TGGTCTCCGCTTCTCCTCTTCTCACTTTCCTCTCTTCTCCTCTGTGTCTTCTTC
TTCTGTAGGAGCTCAAACCACCGTCATCCATAACCCAGTGACGGGATTAAGGTACTGC
[C, T]
CCACTTTCCTCCTCCCGCTTTCCCCAGGCAGGAGGCTCCAGGCCAGGAGAGGCTCTGGG
GCAGCATTTGTGCCAGAGTGAGGGGCAGATGTCCCATGGCCCTGGCCGCCCTCCCCGCA
GTACGGTAGGGCCCCAGTCCGTCTTCGTGGGCAACAACAGGACAGACTGGCTCAGGCCCC
AGGCGCGCCCTTGAGGTGCTTGGCACAGTTGCGCCCGGTCCCCATGTGGCCGACACTCT
CAGACCAGGGCTCTGCGTGTCCACCTACGGCAGGCAGTAGGGCTTCTGAGGTCTGGAG

12603 AGTCTCTCTGCCAGGCTCATCTTGCTGGGAGAAGTGGAGCCCTCATGTGTTGGGGATGCA
GGGTGGCCACAGCACTAGGGTGGCAGGGCCGGCCTCGGACTCCGTGCCAGCCTGTGCTGG
CTGCCGTGAGAATGCACCCTGGTGAGGGGCGCCCTCCAGGGACCAGCACAGAAGTGGGT
GTCTTCTCCGGTCACTGCCGCATGAGGTCCACAGAGCTGGGGCCCTGCAGCCGCCAGAGG
GCATGTCCCCTGAGCCCCCTGGCCTTTAAGCCCCGTGGAAGCAGCCGAGGCAGAGATCAGC
[T, C]
TCAGAGCCTGGGCTGGTCTGTGACACAGGCCACGCCCTGTCCACCTGCCCTCAGCCACGTC
CCACCTATCCTTGCCCGCATCCTGACCCGCTGCCTCCCGTGTTCCTCAGGAGTCTTCTG
ACAGTGCCAATACCACCATAGAGGATGAAGACGCTAAAGGTACCTGCACTTGAGTCTTG
CCCCCCCAGCGGCCCTTGGCATTTGCTGGGTGCTCTTTGAGGTGGGTGGGACTTGGGCAGG
GTCAACTCTCCTGCGACGCCCTAGTTTATGCATGTGTTGAGGGGCTCAGGGACCCTGTAGC

14583 ACATCCTGAGCTCAGTGAGGAGGGGCTCGGGAGCCCCAGAAGCCGAGGGGCCCTGCCCT
GCCCCATCTCCGGCTCCCTTTAGCCCCCTGCCAGCCCCATGTAAGTAGCCTGGGTCTGCT
GCTGTGGGGGTCTGTTGGAGGGCTGGCAACCCCTAGAGGGGCCACTCCAGAGCCGAGG
GCAGGCTGAGCGTGGACCCCTGGCTCCAGCCTCATACCCCACAATCCCTCACTGGGGCTT
TCCAGGGTGGCCCCAGCCCATCGAGCCCCACCTCTTTGTGAGGAGGGCCCTGGACCACTT
[C, T]
CCTGCTCAAGGCCACTGGGCAGGATGGGAGGCCCTGGAGGCTCGGGCCTCAATTCAGTCT
TTCAGGGTGGTGCAGGCCTCACTCCACCTCAGCTTGCGGGCGGGGGGCTCCCTGCTAT
TGAGGCAGGCTCTGATTAGGGCTGATCCAGGGCCCAAGGGGTCTAGAACACGGGACC
CCTCCCACTGGCTCCTCCGCTTGCCGCGCCCTCGTGTGTCTGTCTGCTCATGTTTAC
GTCTCATCTGTTCCACCCAGCCCCAGGGATCTCTGACATCCTGAACTCTGTGAGAAGG

17290 CTGTCCCCTTGTGCCCATCCCCACATCTGCCTCTGTGCCCTCAATCTCTGGCTTGGC
TGTCTGCCCATGGTTTCTCTCCTGCGTGCCCCCGTGCTGCCTTGTGTTACGTCTCGT
CTGTTCCGCCCCAGCCCCAGGATCTCTGACATCCTGAACTCTGTGAGGAGGGGCTCAGG
GACCCAGAAGCCGAGGGCCCCCTCGCCAGTGGGGCCCCCGCCCTGCCATCTCCGACTAT
CCCTGGCCCCCTGCCACCCCATGTAAGTAGCACCTTGAGTGGCCGTGGCAGCGGTGCC
[T, C]
GGAGGGGCTCGGGGCGTGCGAGCCTGGCAGTGGTGTCTGGGAAGGGCCATTCTTGCGGA
GGAGGGCGGGGCACAGGATCCCTCTGCTGGGTCCAGGGAATTGCTTTGAAGCACATGAA
GGTGCCACTGGGTCTCAGAAAATGGAGGTTATGGTTATGAAGTGTGTATGACATATGTGT
ATAGGAAGAGCGTCCGAAAGAGCAGGTTTGTGCGGACCCAGCATTCGCAACCCGAGG
TCCACAGCTTCTCCTGATGGGAGGGGAATGGGTGGCAAAGGCTCTGCGCGTGTGGCAAG

18188 ATCCCAGGGCTGCTGCCACCCCCACCTGTGGGGAGACACCAGACTGGGGGTGGTGTGGAG
ATACTCTTAGAGAAGAGGCTGCTGGGCCACGGGCTCGGCATGGCAGGGCAGTGGCTAGGT
AAGTACTTGAGGGACAGGTGGGGTCTGCTTGCCACCGTCCCCTCTGCAGGCTGGGCCTGG
GGGCTGCTGCAGGCGGCCAGGGCAGAAGGTTGTGGGGAGAGTGAACCCACAGGAGCAGCG
GCTCGAGGAGGGGATGCAGGCTGCAGGCTCAAAGGGGCACTGGATCCACCTGGGTGCC
[C, T]
GAGAGAGCAGGGGGCAGCCCCCTGGAGGGGTACTACCCCCAGAGCTTCTGTGGTGGCTG
AGGACCCCCAGCAGGGGTTGACTGAGGGGATCAGAGGCAAGCAGCTGAGGGGAGAGGCCA
GGTTCCTGTATGCTGATAGGGTGGGGTGCCTGGGCGACCAGAACTCAAGGAGGGAGGCAT
GGGGAGGGGCCCGTGCAGCTGGGGTGGGTGCACCGCAGAGCCTCTGGGAGTGGTCAGA

FIGURE 3, page 13 of 16

ACCCCCGACACCTGCCACTTCTACAGCAGCTCATCTGATTTTAAGGGGCTTGCTGCCCTT
 19911 AGCACGGTTACCACTCTTGATTTGGAACCTTGACCATGCATCTCCTCTTCTGTTACTTCA
 CGCTTTCTCTTCCCATCAACTCCCATTTTAATTACAATTTGTTTAAAAGCACTGCATATT
 ACTTCATTAAACAGAAGATTAGTTTCACTTACCATTAGTGTAAGGTGACTATAGAACCAA
 AGCAGACTGGAAACCAATGACATAATGTATTCTTCTCCATTCCAGCTGCCTGCTGC
 TGTGCGCCTGAGAACCCCTGTGGAGTGGGAGGGGAGCTGTCTCTGTACATTAGAAAGG
 [A, G]
 GGTAACTAAGTGACAGGAGGTGTTTGGGACATGTGGACACCAGACTTCTCTCTTGATGC
 AAGAGGGGAGAGCCAGGCAGCCTAGTGGGGGCTGGCTTGGGGGCTGCTGGAAGGACTGG
 CTACAGGTGGAAGAGAGGTGACACCTGAAGCTTGGGGCCACCTCCAGGAAAGGACAGGTG
 AAAGTGGAGGCATCAGGCAGGGGACAGGCAGGTGCCAGGCAGAGGTGGAGAGGAGGCAG
 GAACATAGCAGCTGGGGCGGGGGCGGGCCCTCAAGTGTATATGCTACTTTCTTGGGGCC
 21328 GCTGGGCACAGTGGCTCATACCTGTAATCCCAGCACTTTGGGAGGCCGAGGTGGGCAGAT
 CACTTGAGGTTAGGAGTTTGAGACCAGCCTGGCCAATATGGTGAAACCTCATCTCCACTA
 AAAATATACACACAAAAATTAGCTGGGTGTGGTGGTGTGCACCTGTAGTTCCAGCTAC
 TCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCTGGGAGTGCAGAGACTGCAGTGAGCCGA
 GATCATGTCACTGCACTCCAGCCCGGTGACAGAGTGAGACTCCATCTAAAAA
 [C, A, G]
 AATTCCTCTCTGGAATTTAGACCACAGACAGGTTGCATGTATGTGGCCGTTGGAGGC
 AGCACTCAGACAAAGAGTGGAAACGTCAACACAGGGCCTGCCTTCTGGTGAAATGGTG
 TCCTGCAGGGCGGGCAGCTGTTTGAGGGCAGGTGTCCAGGTGCGGCCCTGCAGCAGCCTG
 AGGGTGCAGAGCGCAGTGTGGGAGTGCAGAGACTTCCCCACAGGGAGAGTTCCAGG
 AACCTGCTTCCGGTGCCTTCTGGGGTTTGAGTTTTTTCCACGGACGAATTACTTTGAG
 21391 TTGAGGTTAGGAGTTTGAGACCAGCCTGGCCAATATGGTGAAACCTCATCTCCACTAAAA
 ATATACACACAAAAATTAGCTGGGTGTGGTGGTGTGCACCTGTAGTTCCAGCTACTCG
 GGAGGCTGAGGCAGGAGAAATCGCTTGAACCTGGGAGTGCAGAGACTGCAGTGAGCCGAGAT
 CATGTCACTGCACTCCAGCCCGGTGACAGAGTGAGACTCCATCTAAAAA
 [T, C]
 ACTCAGACAAAGAGTGGAAACGTCAACACAGGGCCTGCCTTCTGGTGAAATGGTGTCC
 TGCAGGGCGGGCAGCTGTTTGAGGGCAGGTGTCCAGGTGCGGCCCTGCAGCAGCCTGAGG
 GTCACAGAGCGCAGTGTCTGGGAGTGCAGAGACTTCCCCACAGGGAGAGTTCCAGGAAC
 CTGCTTCCGGTGCCTTCTGGGGTTTGAGTTTTTTCCACGGACGAATTACTTTGAGAAA
 CCACTGTTACTCGTGTGTATAGGTGAGCGTGCCTGTGCATGTGTCTGTGTGTGAGTG
 22588 GCTGCTTCCTCCTCCCCGGCCTCCGGGTGGCCTTGCTGACGGCTCCTTCTCTGAGGCAGG
 TCTCTGCCTTCTCGCTGGTGCCTGCCTCAGTAGCCCCCTCACCAGAGCTGCTGGGTGA
 AGGAAGCACTAAGAACCCAGGCTCGGGAGGAGAGTGGGGCCGGGAAGCTGCAGGGAAGC
 GCAGGGCCAGGCCCTGGTGGGCCCAGGGGCTGGCTCACGGGAGGGCAGGAGGGAGACTGTG
 GCGGACAGCACGTGGGGCCAGGAGGTGACCTCCAAGTGGATTGTGGGTGGGTTTTTTGTG
 [C, T]
 TCTTTCTGCATTTTCCAGGCATTTTGTAAATGTGGATAGAATATTTCTGTTCTTCAAAAT
 ACTTTAGTTAAGAAAAATAAGATGGAAGCTGTTGCACTTGAAAAATGAGGAAGCCACTGGT
 GATGCAGGGGGGCGCGCGGAGAGGACCTTCTGTGCAATAGCGGCAGGAACACGGCATGG
 ATGCAGCTCGCGCTCCCCCAGGCCCTCCCTGGGCTGTGTGGAGGGGTCCGGGGGGAATG
 GGCCAGCGCCAGTGGTCACCTGGCCATGTCTCCCCACAGCCCGGAAGCAGGAGATCATT
 22965 ATAAGATGGAAGCTGTTGCACCTGAAAAATGAGGAAGCCACTGGTGATGCAGGGGGGGCGG
 CGGAGAGGACCTTCTTGCAATAGCGGCAGGAACACGGCATGGATGCAGCTCGCGCTCC
 CCCAGGCCCTCCCCTGGGCTGTGTGGAGGGGTCCGGGGGGAATGGGCCAGCGCCAGTGG
 TCAGAGACCGTGTCTCCCCACAGCCCGGAAGCAGGAGATCATTAAAGACCACGGAGCAGC
 TCATCGAGGCCGTCAACAACGGTGACTTTGAGGCCTACGCGTAGTCCCTGGGGCTGGGG
 [-, G]
 GGGGCTGTGCAGGACAAGGATGTGGGACCCCTTGGGGGGGCTGCTCAGAGTCAGGGGTCC
 ACGGGGCCCCCTCCTCACTTGGATTGTGGCCCCCAGGAAAAATCTGTGACCCAGGGCTGACCT
 CGTTTGAGCCTGAAGCACTGGGCAACCTGGTTGAAGGGATGGAATCCACAGATTCTACT
 TCGAGAACCCTGAGTGAGGAAGCCCGGGTGGGCATGAGGGGGCGGTGCCCCCAGGAGAGC
 CTCTCGGCCCTCCAGGGACAGCATGGTGGCTGCCTATGGAAGCCCTGTCCCCTCTGTG
 23498 CCCGCCAGAGGCCATACCCAGCCCCCAGAATCCCACTCTTGAGGGGGCCCATGCTGCTCC

FIGURE 3, page 14 of 16

CAGGAGAGCCGAGCCTCCCCAATAAGGGGAGTTGAGAGAGGGAAAGGATTAGGCTGGTGG
GGTGAAGACGGGCACACAGGCAGTCATGGTAACCCGAGACCCCCGCCCCGCTGCTGTC
CACAGTGCTGGCCAAGAACAGCAAGCC

[G, A]

ATCCACACGACCATCCTGAACCCACACGTGCACGTCAATTGGAGAGGATGCCGCTGCATC
GCTTACATCCGGCTCACGCAGTACATTGACGGGCAGGGCCGGCCCCGCACACAGCCAGTCT
GAGGAGACCCGCGTGTGGCACC GCCCGACGGCAAGTGGCAGAACGTGCACTTCCACTGC
TCGGGCGCGCCTGTGGCCCCGCTGCAG

23663

GCCTCCCCAATAAGGGGAGTTGAGAGAGGGAAAGGATTAGGCTGGTGGGTGGAAGACGG
GCACCAGGGCAGTCATGGTAACCCGAGACCCCCGCCCCGCTGCTGTCCACAGTGCTGGC
CAAGAACAGCAAGCCGATCCACACGACCATCCTGAACCCACACGTGCACGTCAATTGGAGA
GGATGCCGCTGCATCGCTTACATCCGGCTCACGCAGTACATTGACGGGCAGGGCCGGCC
CCGCACACAGCCAGTCTGAGGAGACCCGCGTGTGGCACC GCCCGACGGCAAGTGGCAGAA

[T, C]

GTGCACCTTCCACTGCTCGGGCGCGCCTGTGGCCCCGCTGCAGTGAAGGTGAGTGTCTGT
GCTAAGTGACAGCTGGGGCAGAGGGGTGGCGGTGGTGTGAGTGGCTGCAGCCTGGGGAGG
CGATGGGGAGCGGTGGGGCCTGTGGCAGAGCCCATGCCTGGGAAGTCCCTGAGCTTTCCT
GGTGAGGCCACAGGAATGATGTCAAATTAGGGACCACGGCAGGCTGGGTGTGGCAGGCCT
CCCCAGAGGACTGGGGAGCTGGTGAGGGCCTGAGCAGTCCACACTGGCCAGAGCTGGGTG

25427

TGTGGCAAGAGGACTCTGCCTGGGCTGGCCCCCTCCTGTGTGAGGTGTCTGTCCCTTCT
CTGCTGGCCAGCAGCAGATGCCTGGCAGCTCCCAACCTGTTTCCGCCCCCTCGGCCCTC
CCCCAGCCTGTTCCGCTTCTCTGCAGCCCGCAAGGGGGAGCAGACTTTTGACAAAGGACT
GCGGGCCTCGCTCAAGTCCCTGAGCCCCCAGCTGAAGCTGGGAGGGGAGGCCAGGCTTTG
TGTCTGGGCATATTCGTCTGCTGATGGGGTTTGGGGAAGCCTGGGGCTTGGGGTTTGGTC

[A, G]

GGTGGTGACAGCTAGTGGCAGAGCGGGATCAGAGGTGGTGGCTGCCAGCTTCTGGGCTGA
GACAAGGGTCTGTGCAGGGGTTTACTGAAGTGGGAGTGCCCTTGGGAATCTGGGCCGGGAG
CAGAAGGGAGCAAAAGCTACAGTGGGAGCCAGCCTAGGGCACATGGGAGGCGTGAGGGCA
GTGCTGCCCGTGCAGTGTGAGGTGTGCCAGTGCCTTGGCGGGCTGCAGTGCCTGTGAGGG
CACCTTCTAGGTGGGCCAGGGATGCAGCTATGGAGATAAGGCGGGCTGGGGACAGAAACA

27727

GCAAACCTCTTAGGTTGGAGTAAGGAGTAACCCCTGCCAAGTTTCTCCTGTCTCAGGCT
CCACCCACCACTATGCTGCCTGGCCCCATGGGGCACACGCTCAGGCCCAGCCTGGGAAA
GCAACTGCACCTGCCTGTGCTATGCTGGCCCTTCTCAGCCTCAATGCCCTCCTCCCTCCC
CGACGCACCCCTCGTGGCCCCCGCTGGGCCCCCTGATGCACCCCTCATGTCTCCATGGCAAC
CTGCTCAGAGTGTGGCCCTGCCCTTGGCTCCCTCCACACCTGTGTCCAGGCAGTGCCA

[C, T]

GGCACCTTTCCTAACAGAAGGATGGGCTTCAAAACAGTCCCAGACACTAAACACACCTGC
ATTTTGGGTCCAAGTAACCTTCTGACAAGACGAGTGCCCTACACACCCTCAGTCCCTATCC
ACTATGGGCAAGGAGCCTGAAGGATCCCCCAGAACTGGCTAAAGCCCTCAGTCTCCTCCT
CCACCCCTGAGCACCTTCACGCGGCAGAGTGGCCCTGGATGTGAGCTTCTTGCTCCCCATG
GTCTGCACCTGGACAGGTGCTCTCAGGTGTGTGGGTGGGCAGGTGGCAGGTCCCAAGAGC

27834

CCAGCCTGGGAAAGCAACTGCACCTGCCTGTGCTATGCTGGCCCTTCTCAGCCTCAATGC
CCTCCTCCCTCCCCGACGCACCCCTCGTGGCCCCCGCTGGGCCCCCTGATGCACCCCTCATG
TCTCCATGGCAACCTGCTCAGAGTGTGGCCCTGCCCTTGGCTCCCCCTCCACACCTGTGTC
CCAGGCAGTGCCACGGCACTTTCCTAAACAGAAGGATGGGCTTCAAAACAGTCCCAGACA
CTAAACACACCTGCATTTTGGGTCCAAGTAACCTTCTGACAAGACGAGTGCCCCCTACACAC

[T, C]

CTCAGTCCCTATCCACTATGGGCAAGGAGCCTGAAGGATCCCCCAGAACTGGCTAAAGCCC
TCAGTCTCCTCCTCCACCCCTGAGCACCTTCACGCGGCAGAGTGGCCCTGGATGTGAGCTT
CTTGCTCCCCATGGTCTGCACCTGGACAGGTGCTCTCAGGTGTGTGGGTGGGCAGGTGGC
AGGTCCCAGAGCCAGGTGCAAAGAATCTAGGCCAGTGGCCACGAGTGTGCTGAGTGTCTG
TCCCCAGCATGGTATCTAGGGCTCCACTTGCCTATCAGCTGTAATCGGAGGAGGCTTTC

FIGURE 3, page 15 of 16

AAGAATCTAGGCCAGTGCACACGAGTGTCTGTCAGTGTCTGTCCCCAGCATGGTATCTAGGG
 CTCCACTTGCCTATCAGCTGTAATCGGAGGAGGCTTTCCAGGCCAGGCCTCCCCAGGAA
 GGCTGCAGGCACCTGCGGATCGTGCGCCCTCACATGCATTATTCCTGAGGCCCTTCTGCAG
 ATGCCATCAGGGCAGCAACTCTGATGAGGTATTAGGGCACAGCACACAGGGCTAAGCCAC
 CCTGTACTGGGCCAAGCGCTACAGGCCAAAAGGACACCACCGACGGGCATTTCATTTCATC
 [G,A]
 CTTTATTATTTATATATTTTGTAGAGGGAGCCTCACTGTGCGCCAGGCTGGAGTGCAG
 TGGCGCGATCTTGGCTCACTGCAACTTCTCCCTCCGGGTTC

1997		1998		1999		2000		2001		2002		2003		2004		2005		2006		2007		2008		2009		2010		2011		2012		2013		2014		2015		2016		2017		2018		2019		2020		2021		2022		2023		2024		2025		2026		2027		2028		2029		2030		2031		2032		2033		2034		2035		2036		2037		2038		2039		2040		2041		2042		2043		2044		2045		2046		2047		2048		2049		2050		2051		2052		2053		2054		2055		2056		2057		2058		2059		2060		2061		2062		2063		2064		2065		2066		2067		2068		2069		2070		2071		2072		2073		2074		2075		2076		2077		2078		2079		2080		2081		2082		2083		2084		2085		2086		2087		2088		2089		2090		2091		2092		2093		2094		2095		2096		2097		2098		2099		2100	
1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100																																																																																																								